

Schultz
DA1700906
Seq. ID 3

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 17, 2002, 21:26:35 ; Search time 1890.87 Seconds
(without alignments)
254.544 Million cell updates/sec

Title: US-09-700-906A-3

Perfect score: 23

Sequence: 1 accaggcgtctcgtggccacat 23

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 708260

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_htg.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vl.*

15: em_ba.*

16: em_fun.*

17: em_hum.*

18: em_in.*

19: em_mu.*

20: em_om.*

21: em_or.*

22: em_ov.*

23: em_pat.*

24: em_ph.*

25: em_pl.*

26: em_ro.*

27: em_sts.*

28: em_un.*

29: em_vl.*

30: em_htg_hum.*

31: em_htg_inv.*

32: em_htg_other.*

33: em_htgo_inv.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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220	11	47.8	21	6	AX095679 Sequence	AX095679 Sequence	c 293	10.8	47.0	24	6	A57385 Sequence 22
221	11	47.8	23	6	AR088242 Sequence	AR088242 Sequence	c 294	10.8	47.0	24	6	AR028445 Sequence
c-222	11	47.8	24	6	A92197 Sequence 31	A92197 Sequence 31	c 295	10.8	47.0	24	6	AR075384 Sequence
c 223	11	47.8	24	6	BD009172 Herbicide	BD009172 Herbicide	c 296	10.8	47.0	24	6	AX015220 Sequence
224	11	47.8	25	6	A48832 Sequence 24	A48832 Sequence 24	c 297	10.8	47.0	24	6	AX030702 Sequence
225	11	47.8	25	6	AX279054 Sequence	AX279054 Sequence	c 298	10.8	47.0	24	6	AX055030 Sequence
226	11	47.8	26	6	AR019480 Sequence	AR019480 Sequence	c 299	10.8	47.0	24	6	AX166504 Sequence
227	11	47.8	26	6	AR029003 Sequence	AR029003 Sequence	c 300	10.8	47.0	24	6	AX174822 Sequence
228	11	47.8	26	6	AR065941 Sequence	AR065941 Sequence	c 301	10.8	47.0	24	6	AX175503 Sequence
229	11	47.8	26	6	AX023675 Sequence	AX023675 Sequence	c 302	10.8	47.0	24	6	AX175511 Sequence
230	11	47.8	27	6	AR000011 Sequence	AR000011 Sequence	c 303	10.8	47.0	24	6	AX288328 Sequence
231	11	47.8	27	6	AR006779 Sequence	AR006779 Sequence	c 304	10.8	47.0	24	6	AX289475 Sequence
232	11	47.8	27	6	AR015967 Sequence	AR015967 Sequence	c 305	10.8	47.0	24	6	AX289529 Sequence
233	11	47.8	27	6	AR060924 Sequence	AR060924 Sequence	c 306	10.8	47.0	24	6	AX290618 Sequence
234	11	47.8	27	6	AR135387 Sequence	AR135387 Sequence	c 307	10.8	47.0	24	6	AX291134 Sequence
235	11	47.8	27	6	AX032419 Sequence	AX032419 Sequence	c 308	10.8	47.0	24	6	AX291661 Sequence
c 236	11	47.8	27	6	AX034682 Sequence	AX034682 Sequence	c 309	10.8	47.0	24	6	AX291773 Sequence
c 237	11	47.8	27	6	AX343650 Sequence	AX343650 Sequence	c 310	10.8	47.0	24	6	AX291849 Sequence
238	11	47.8	27	6	BD004718 Chimeric	BD004718 Chimeric	c 311	10.8	47.0	24	6	AX298290 Sequence
239	11	47.8	27	6	I40980 Sequence 9	I40980 Sequence 9	c 312	10.8	47.0	24	6	AX300720 Sequence
240	11	47.8	27	6	I71291 Sequence 29	I71291 Sequence 29	c 313	10.8	47.0	24	6	AX300929 Sequence
241	11	47.8	28	6	E40799 Antihuman F	E40799 Antihuman F	c 314	10.8	47.0	24	6	BD006697 Transport
c 242	11	47.8	29	6	AX104378 Sequence	AX104378 Sequence	c 315	10.8	47.0	24	6	E14845 PCR primer.
c 243	11	47.8	29	6	AX355803 Sequence	AX355803 Sequence	c 316	10.8	47.0	25	6	AX349971 Sequence
c 244	11	47.8	30	6	A22349 H.sapiens H	A22349 H.sapiens H	c 317	10.8	47.0	26	6	AR090256 Sequence
c 245	11	47.8	30	6	AR041112 Sequence	AR041112 Sequence	c 318	10.8	47.0	26	6	E17233 Linker. 7/1
c 246	11	47.8	30	6	AR066006 Sequence	AR066006 Sequence	c 319	10.8	47.0	27	6	AR000575 Sequence
c 247	11	47.8	30	6	AR072748 Sequence	AR072748 Sequence	c 320	10.8	47.0	27	6	AX063382 Sequence
248	11	47.8	30	10	S86291 TCR V beta	S86291 TCR V beta	c 321	10.8	47.0	27	6	BD003627 A polynuc
249	11	47.8	31	6	AX248477 Sequence	AX248477 Sequence	c 322	10.8	47.0	28	6	AR049468 Sequence
250	11	47.8	31	6	AX248707 Sequence	AX248707 Sequence	c 323	10.8	47.0	28	6	AR051619 Sequence
251	11	47.8	31	6	AX248814 Sequence	AX248814 Sequence	c 324	10.8	47.0	29	6	A57691 Sequence 1
c 252	11	47.8	31	6	E02911 oligonucleo	E02911 oligonucleo	c 325	10.8	47.0	29	6	A76939 Sequence 1
c 253	11	47.8	32	6	AR125498 Sequence	AR125498 Sequence	c 326	10.8	47.0	29	6	AR070077 Sequence
c 254	11	47.8	32	6	AX093107 Sequence	AX093107 Sequence	c 327	10.8	47.0	30	6	A14220 oligonucleo
c 255	11	47.8	33	6	AR004384 Sequence	AR004384 Sequence	c 328	10.8	47.0	30	6	AR063744 Sequence
256	11	47.8	33	6	AR097175 Sequence	AR097175 Sequence	c 329	10.8	47.0	30	6	AR084491 Sequence
c 257	11	47.8	33	6	AR125497 Sequence	AR125497 Sequence	c 330	10.8	47.0	30	6	AR107271 Sequence
258	11	47.8	33	6	AR130673 Sequence	AR130673 Sequence	c 331	10.8	47.0	30	6	AR107272 Sequence
c 259	11	47.8	33	6	AR172022 Sequence	AR172022 Sequence	c 332	10.8	47.0	30	6	AR159571 Sequence
c 260	11	47.8	33	6	AR134751 Sequence	AR134751 Sequence	c 333	10.8	47.0	30	6	AR172390 Sequence
261	11	47.8	33	6	I82859 Sequence 38	I82859 Sequence 38	c 334	10.8	47.0	30	6	I30107 Sequence 29
c 262	11	47.8	34	6	A93643 Sequence 2	A93643 Sequence 2	c 335	10.8	47.0	31	6	AR071456 Sequence
c 263	11	47.8	34	6	AR176284 Sequence	AR176284 Sequence	c 336	10.8	47.0	31	6	AX249666 Sequence
264	11	47.8	35	6	I40076 Sequence 35	I40076 Sequence 35	c 337	10.8	47.0	31	6	AX280677 Sequence
c 265	11	47.8	35	6	I40078 Sequence 37	I40078 Sequence 37	c 338	10.8	47.0	31	6	AX280678 Sequence
c 266	11	47.8	35	9	S72578 TCR delta =	S72578 TCR delta =	c 339	10.8	47.0	31	6	BD002908 Gene comp
c 267	11	47.8	36	6	A63365 Sequence 20	A63365 Sequence 20	c 340	10.8	47.0	31	6	I41399 Sequence 2
c 268	11	47.8	36	6	AX092228 Sequence	AX092228 Sequence	c 341	10.8	47.0	32	6	AX280679 Sequence
c 269	11	47.8	36	6	AX224672 Sequence	AX224672 Sequence	c 342	10.8	47.0	32	6	AX280680 Sequence
270	11	47.8	40	6	AR078066 Sequence	AR078066 Sequence	c 343	10.8	47.0	32	6	E36188 Upstream re
271	11	47.8	40	6	E35647 Detection o	E35647 Detection o	c 344	10.8	47.0	33	6	AR071445 Sequence
c 272	11	47.8	41	6	AR078065 Sequence	AR078065 Sequence	c 345	10.8	47.0	33	6	AX317353 Sequence
273	11	47.8	41	6	E35646 Detection o	E35646 Detection o	c 346	10.8	47.0	33	6	AX317354 Sequence
c 274	11	47.8	42	6	AX044068 Sequence	AX044068 Sequence	c 347	10.8	47.0	35	6	AR099775 Sequence
c 275	11	47.8	45	6	A68111 Sequence 16	A68111 Sequence 16	c 348	10.8	47.0	36	6	AX077721 Sequence
c 276	11	47.8	45	6	A68111 Sequence 20	A68111 Sequence 20	c 349	10.8	47.0	36	6	AX136876 Sequence
c 277	11	47.8	45	6	E22037 Seven-pass	E22037 Seven-pass	c 350	10.8	47.0	36	6	AX136878 Sequence
c 278	11	47.8	47	6	AX044058 Sequence	AX044058 Sequence	c 351	10.8	47.0	36	6	E27482 Novel dnase
c 279	11	47.8	48	6	AR024316 Sequence	AR024316 Sequence	c 352	10.8	47.0	37	6	AX211299 Sequence
280	11	47.8	48	6	AR045169 Sequence	AR045169 Sequence	c 353	10.8	47.0	37	6	AX211300 Sequence
281	11	47.8	48	6	BD011393 Chimeric	BD011393 Chimeric	c 354	10.8	47.0	38	9	HUMTCRVJ40
282	11	47.8	48	6	E43863 Chimeric an	E43863 Chimeric an	c 355	10.8	47.0	39	6	AR001559 Sequence
c 283	11	47.8	49	6	I05520 Sequence 8	I05520 Sequence 8	c 356	10.8	47.0	39	6	AR086367 Sequence
c 284	10.8	47.0	19	6	AX129198 Sequence	AX129198 Sequence	c 357	10.8	47.0	39	6	AR104976 Sequence
c 285	10.8	47.0	20	6	AX021609 Sequence	AX021609 Sequence	c 358	10.8	47.0	39	6	AR145839 Sequence
c 286	10.8	47.0	20	6	AX253336 Sequence	AX253336 Sequence	c 359	10.8	47.0	39	6	E35283 Assay of Ch
c 287	10.8	47.0	20	6	AX292961 Sequence	AX292961 Sequence	c 360	10.8	47.0	40	6	A67373 Sequence 12
c 288	10.8	47.0	20	6	AX294855 Sequence	AX294855 Sequence	c 361	10.8	47.0	40	6	A90919 Sequence 26
c 289	10.8	47.0	20	6	AX296406 Sequence	AX296406 Sequence	c 362	10.8	47.0	40	6	AX202304 Sequence
290	10.8	47.0	20	6	I12670 Sequence 80	I12670 Sequence 80	c 363	10.8	47.0	40	6	I92643 Sequence 17
291	10.8	47.0	21	6	AR177624 Sequence	AR177624 Sequence	c 364	10.8	47.0	41	9	S81437 T cell anti
c 292	10.8	47.0	23	6	E07721 Primer. 9/1	E07721 Primer. 9/1	c 365	10.8	47.0	42	6	AR100925 Sequence

c 366	10.8	47.0	43	6	AX008489	Sequence	AX008489	Sequence	c 439	10.6	46.1	22	6	AR012666	AR012666	Sequence
c 367	10.8	47.0	43	6	AX085142	Sequence	AX085142	Sequence	c 440	10.6	46.1	22	6	I25032	I25032	Sequence 6
c 368	10.8	47.0	44	6	AX086375	Sequence	AX086375	Sequence	c 441	10.6	46.1	22	6	I30494	I30494	Sequence 6
c 369	10.8	47.0	44	9	HUMFTBB	MI5899	Human nucle		c 442	10.6	46.1	22	6	I72556	I72556	Sequence 5
c 370	10.8	47.0	45	6	AR021427	Sequence	AR021427	Sequence	c 443	10.6	46.1	23	6	AR051700	AR051700	Sequence
c 371	10.8	47.0	45	6	AR021428	Sequence	AR021428	Sequence	c 444	10.6	46.1	23	6	AR069972	AR069972	Sequence
c 372	10.8	47.0	45	6	AR042989	Sequence	AR042989	Sequence	c 445	10.6	46.1	23	6	AX322619	AX322619	Sequence
c 373	10.8	47.0	45	6	AR042990	Sequence	AR042990	Sequence	c 446	10.6	46.1	23	6	I18233	I18233	Sequence 15
c 374	10.8	47.0	45	6	AR086374	Sequence	AR086374	Sequence	c 447	10.6	46.1	24	6	AX290711	AX290711	Sequence
c 375	10.8	47.0	45	6	AR117917	Sequence	AR117917	Sequence	c 448	10.6	46.1	24	6	AX291106	AX291106	Sequence
c 376	10.8	47.0	45	6	AR161323	Sequence	AR161323	Sequence	c 449	10.6	46.1	24	6	AX291628	AX291628	Sequence
c 377	10.8	47.0	45	6	AR161324	Sequence	AR161324	Sequence	c 450	10.6	46.1	24	6	E13447	E13447	PCR primer
c 378	10.8	47.0	45	6	I43968	Sequence 59	I43968	Sequence 59	c 451	10.6	46.1	25	6	AR051699	AR051699	Sequence
c 379	10.8	47.0	45	6	I43969	Sequence 60	I43969	Sequence 60	c 452	10.6	46.1	25	6	AX039274	AX039274	Sequence
c 380	10.8	47.0	45	6	I62980	Sequence 10	I62980	Sequence 10	c 453	10.6	46.1	25	6	I18232	I18232	Sequence 14
c 381	10.8	47.0	45	6	I62981	Sequence 10	I62981	Sequence 10	c 454	10.6	46.1	26	6	AR106358	AR106358	Sequence
c 382	10.8	47.0	45	6	I88733	Sequence 10	I88733	Sequence 10	c 455	10.6	46.1	27	6	AR07708	AR07708	Synthetic n
c 383	10.8	47.0	45	6	I88734	Sequence 10	I88734	Sequence 10	c 456	10.6	46.1	27	6	A10007	A10007	Nucleotide
c 384	10.8	47.0	46	6	A42682	Sequence 14	A42682	Sequence 14	c 457	10.6	46.1	27	6	A81445	A81445	Sequence 8
c 385	10.8	47.0	46	6	A74862	Sequence 54	A74862	Sequence 54	c 458	10.6	46.1	27	6	A81614	A81614	Sequence 8
c 386	10.8	47.0	46	6	A77841	Sequence 54	A77841	Sequence 54	c 459	10.6	46.1	27	6	AR017903	AR017903	Sequence
c 387	10.8	47.0	46	6	AR043537	Sequence	AR043537	Sequence	c 460	10.6	46.1	27	6	AR024195	AR024195	Sequence
c 388	10.8	47.0	46	6	AR063856	Sequence	AR063856	Sequence	c 461	10.6	46.1	27	6	BD005344	BD005344	Enhanced
c 389	10.8	47.0	46	6	AR075820	Sequence	AR075820	Sequence	c 462	10.6	46.1	27	6	I15110	I15110	Sequence 13
c 390	10.8	47.0	46	6	AR098732	Sequence	AR098732	Sequence	c 463	10.6	46.1	29	6	AX351506	AX351506	Sequence
c 391	10.8	47.0	46	6	AR112324	Sequence	AR112324	Sequence	c 464	10.6	46.1	30	6	AX047007	AX047007	Sequence
c 392	10.8	47.0	46	6	E30453	E30453	Method for		c 465	10.6	46.1	30	6	AX047016	AX047016	Sequence
c 393	10.8	47.0	46	6	E32363	E32363	Method for		c 466	10.6	46.1	31	10	MHNF113B	X66552	Mus muscula
c 394	10.8	47.0	46	6	E33634	E33634	Detection o		c 467	10.6	46.1	31	6	AX001316	AX001316	Sequence
c 395	10.8	47.0	46	6	E35691	E35691	Detection a		c 468	10.6	46.1	31	6	E36252	E36252	Human semap
c 396	10.8	47.0	46	6	I87188	Sequence 14	I87188	Sequence 14	c 469	10.6	46.1	32	6	AR075029	AR075029	Sequence
c 397	10.8	47.0	47	10	S82866S2	S82867	Apod-apolip		c 470	10.6	46.1	32	6	AR118493	AR118493	Sequence
c 398	10.8	47.0	48	6	AR049475	Sequence	AR049475	Sequence	c 471	10.6	46.1	33	6	AR064939	AR064939	Sequence
c 399	10.8	47.0	48	6	AR051626	Sequence	AR051626	Sequence	c 472	10.6	46.1	33	6	AR097192	AR097192	Sequence
c 400	10.8	47.0	48	9	HSU14064	Human T cel	U14064	Human T cel	c 473	10.6	46.1	33	6	AR130690	AR130690	Sequence
c 401	10.8	47.0	49	6	AX019736	Sequence	AX019736	Sequence	c 474	10.6	46.1	33	6	AR172039	AR172039	Sequence
c 402	10.8	47.0	50	6	A14174	vectorrete	A14174	vectorrete	c 475	10.6	46.1	35	6	AR043567	AR043567	Sequence
c 403	10.8	47.0	50	6	A14176	A14176	vectorrete		c 476	10.6	46.1	35	6	AX058076	AX058076	Sequence
c 404	10.8	47.0	50	6	A14178	A14178	vectorrete		c 477	10.6	46.1	36	6	A33740	A33740	Synthetic D
c 405	10.8	47.0	50	6	A14198	A14198	specific ve		c 478	10.6	46.1	36	6	A33741	A33741	Synthetic D
c 406	10.8	47.0	50	6	AR032767	Sequence	AR032767	Sequence	c 479	10.6	46.1	36	6	AR068333	AR068333	Sequence
c 407	10.8	47.0	50	6	AX000366	Sequence	AX000366	Sequence	c 480	10.6	46.1	36	6	AX019533	AX019533	Sequence
c 408	10.8	47.0	50	6	AX000367	Sequence	AX000367	Sequence	c 481	10.6	46.1	36	6	AX268888	AX268888	Sequence
c 409	10.8	47.0	50	6	AX160500	Sequence	AX160500	Sequence	c 482	10.6	46.1	36	6	AX268894	AX268894	Sequence
c 410	10.8	47.0	50	6	AX199682	Sequence	AX199682	Sequence	c 483	10.6	46.1	36	6	AX317301	AX317301	Sequence
c 411	10.8	47.0	50	6	E40785	E40785	Antihuman F		c 484	10.6	46.1	36	6	AX317314	AX317314	Sequence
c 412	10.8	47.0	50	6	I29507	I29507	Sequence 37		c 485	10.6	46.1	36	6	AX317480	AX317480	Sequence
c 413	10.8	47.0	50	6	I91181	Sequence 37	I91181	Sequence 37	c 486	10.6	46.1	36	6	I65465	I65465	Sequence 1
c 414	10.6	46.1	18	6	AR052908	Sequence	AR052908	Sequence	c 487	10.6	46.1	38	6	A28707	A28707	Dia 5' prim
c 415	10.6	46.1	18	6	AR054271	Sequence	AR054271	Sequence	c 488	10.6	46.1	38	6	I19043	I19043	Sequence 3
c 416	10.6	46.1	18	6	AR054473	Sequence	AR054473	Sequence	c 489	10.6	46.1	39	6	AR004622	AR004622	Sequence
c 417	10.6	46.1	18	6	AR163072	Sequence	AR163072	Sequence	c 490	10.6	46.1	39	6	I65468	I65468	Sequence 4
c 418	10.6	46.1	18	6	E01966	E01966	Variant ind		c 491	10.6	46.1	40	6	AR004621	AR004621	Sequence
c 419	10.6	46.1	18	6	I24671	I24671	Sequence 55		c 492	10.6	46.1	40	6	AR105362	AR105362	Sequence
c 420	10.6	46.1	18	6	I25268	I25268	Sequence 55		c 493	10.6	46.1	40	6	AR135207	AR135207	Sequence
c 421	10.6	46.1	19	6	AR157491	Sequence	AR157491	Sequence	c 494	10.6	46.1	40	6	AR135220	AR135220	Sequence
c 422	10.6	46.1	19	6	AX166874	Sequence	AX166874	Sequence	c 495	10.6	46.1	40	6	AR146703	AR146703	Sequence
c 423	10.6	46.1	20	6	AR050659	Sequence	AR050659	Sequence	c 496	10.6	46.1	40	6	AR146716	AR146716	Sequence
c 424	10.6	46.1	20	6	AR124491	Sequence	AR124491	Sequence	c 497	10.6	46.1	40	6	AR152274	AR152274	Sequence
c 425	10.6	46.1	20	6	AR126630	Sequence	AR126630	Sequence	c 498	10.6	46.1	40	6	AR152287	AR152287	Sequence
c 426	10.6	46.1	20	6	AX056719	Sequence	AX056719	Sequence	c 499	10.6	46.1	40	6	AR157812	AR157812	Sequence
c 427	10.6	46.1	20	6	AX295344	Sequence	AX295344	Sequence	c 500	10.6	46.1	40	6	AR157825	AR157825	Sequence
c 428	10.6	46.1	20	6	AX295739	Sequence	AX295739	Sequence	c 501	10.6	46.1	42	6	AR154192	AR154192	Sequence
c 429	10.6	46.1	20	6	E08449	E08449	DNA fragmen		c 502	10.6	46.1	42	6	AR175519	AR175519	Sequence
c 430	10.6	46.1	20	6	E08910	E08910	Oligonucleo		c 503	10.6	46.1	42	6	AX268903	AX268903	Sequence
c 431	10.6	46.1	20	6	E37917	E37917	Nucleic aci		c 504	10.6	46.1	42	6	AX268907	AX268907	Sequence
c 432	10.6	46.1	20	6	I12598	I12598	Sequence 8		c 505	10.6	46.1	42	9	HUMTCCVJ36	L39503	Homo saplen
c 433	10.6	46.1	21	6	AR069973	Sequence	AR069973	Sequence	c 506	10.6	46.1	45	6	AR007208	AR007208	Sequence
c 434	10.6	46.1	21	6	AX095147	Sequence	AX095147	Sequence	c 507	10.6	46.1	45	6	AR048111	AR048111	Sequence
c 435	10.6	46.1	21	6	AX096280	Sequence	AX096280	Sequence	c 508	10.6	46.1	45	6	AR054215	AR054215	Sequence
c 436	10.6	46.1	21	6	AX201232	Sequence	AX201232	Sequence	c 509	10.6	46.1	45	6	AR063976	AR063976	Sequence
c 437	10.6	46.1	22	6	A87888	Sequence 36	A87888	Sequence 36	c 510	10.6	46.1	45	6	AR107743	AR107743	Sequence
c 438	10.6	46.1	22	6	A89855	Sequence 36	A89855	Sequence 36	c 511	10.6	46.1	45	6	AR117920	AR117920	Sequence

c 512	10.6	46.1	46	6	AR032532	AR032532 Sequence	c 585	10.4	45.2	27	6	E06045	E06045 Linker. 9/1
c 513	10.6	46.1	46	6	I29272	I29272 Sequence 14	c 586	10.4	45.2	27	6	I21793	I21793 Sequence 7
c 514	10.6	46.1	46	6	I90946	I90946 Sequence 14	c 587	10.4	45.2	27	6	I57362	I57362 Sequence 5
c 515	10.6	46.1	47	6	AR027754	AR027754 Sequence	c 588	10.4	45.2	27	6	I66408	I66408 Sequence 6
c 516	10.6	46.1	47	6	AR029158	AR029158 Sequence	c 589	10.4	45.2	27	6	I66409	I66409 Sequence 7
c 517	10.6	46.1	47	6	AR036542	AR036542 Sequence	c 590	10.4	45.2	28	6	AX280309	AX280309 Sequence
c 518	10.6	46.1	47	6	AR096075	AR096075 Sequence	c 591	10.4	45.2	29	6	AX022542	AX022542 Sequence
c 519	10.6	46.1	47	6	AR111942	AR111942 Sequence	c 592	10.4	45.2	29	6	AX022543	AX022543 Sequence
c 520	10.6	46.1	47	6	AR124839	AR124839 Sequence	c 593	10.4	45.2	29	6	AX175194	AX175194 Sequence
c 521	10.6	46.1	47	6	AR135287	AR135287 Sequence	c 594	10.4	45.2	29	6	AX280510	AX280510 Sequence
c 522	10.6	46.1	47	6	AR141340	AR141340 Sequence	c 595	10.4	45.2	29	6	E39279	E39279 Labeled pri
c 523	10.6	46.1	47	6	AR157495	AR157495 Sequence	c 596	10.4	45.2	29	6	E39280	E39280 Labeled pri
c 524	10.6	46.1	47	6	I31656	I31656 Sequence 7	c 597	10.4	45.2	30	6	AR051649	AR051649 Sequence
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c 526	10.6	46.1	48	6	AX164151	AX164151 Sequence	c 599	10.4	45.2	30	6	AX151765	AX151765 Sequence
c 527	10.6	46.1	49	6	AX5046	AX5046 Sequence 21	c 600	10.4	45.2	30	6	AX350348	AX350348 Sequence
c 528	10.6	46.1	49	6	AR029662	AR029662 Sequence	c 601	10.4	45.2	30	6	BD005219	BD005219 Novel yea
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c 532	10.4	45.2	15	6	AR033413	AR033413 Sequence	c 605	10.4	45.2	31	6	AX248867	AX248867 Sequence
c 533	10.4	45.2	15	6	AR113235	AR113235 Sequence	c 606	10.4	45.2	31	6	AX249286	AX249286 Sequence
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c 536	10.4	45.2	19	6	AX278625	AX278625 Sequence	c 609	10.4	45.2	31	6	E06839	E06839 Oligonucleo
c 537	10.4	45.2	20	6	AR011700	AR011700 Sequence	c 610	10.4	45.2	32	6	A39467	A39467 Sequence 26
c 538	10.4	45.2	20	6	AR092300	AR092300 Sequence	c 611	10.4	45.2	32	6	A98587	A98587 Sequence 12
c 539	10.4	45.2	20	6	AR119517	AR119517 Sequence	c 612	10.4	45.2	32	6	AR001358	AR001358 Sequence
c 540	10.4	45.2	20	6	AR122434	AR122434 Sequence	c 613	10.4	45.2	32	6	AR028335	AR028335 Sequence
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c 542	10.4	45.2	20	6	AX297314	AX297314 Sequence	c 615	10.4	45.2	32	6	AR044853	AR044853 Sequence
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c 545	10.4	45.2	21	6	AX038334	AX038334 Sequence	c 618	10.4	45.2	32	6	AR070855	AR070855 Sequence
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c 547	10.4	45.2	21	6	AX189549	AX189549 Sequence	c 620	10.4	45.2	32	6	AR085189	AR085189 Sequence
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c 550	10.4	45.2	22	6	AR173689	AR173689 Sequence	c 623	10.4	45.2	32	6	AX040345	AX040345 Sequence
c 551	10.4	45.2	22	6	AX038335	AX038335 Sequence	c 624	10.4	45.2	32	6	AX020204	AX020204 Sequence
c 552	10.4	45.2	22	6	AX107493	AX107493 Sequence	c 625	10.4	45.2	32	6	E13335	E13335 Primer. 6/1
c 553	10.4	45.2	22	6	E31632	E31632 Method for	c 626	10.4	45.2	32	6	E38136	E38136 Method for
c 554	10.4	45.2	22	6	E31642	E31642 Method for	c 627	10.4	45.2	32	6	I24933	I24933 Sequence 5
c 555	10.4	45.2	22	6	E31643	E31643 Method for	c 628	10.4	45.2	32	6	I33893	I33893 Sequence 1
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c 557	10.4	45.2	23	6	AX038336	AX038336 Sequence	c 630	10.4	45.2	32	6	I35717	I35717 Sequence 6
c 558	10.4	45.2	24	6	A69677	A69677 Sequence 7	c 631	10.4	45.2	32	23	E11416	E11416 Primer. 9/2
c 559	10.4	45.2	24	6	AR174006	AR174006 Sequence	c 632	10.4	45.2	33	6	A45492	A45492 Sequence 21
c 560	10.4	45.2	24	6	AX038337	AX038337 Sequence	c 633	10.4	45.2	33	6	AR004355	AR004355 Sequence
c 561	10.4	45.2	24	6	AX111721	AX111721 Sequence	c 634	10.4	45.2	33	6	AR004396	AR004396 Sequence
c 562	10.4	45.2	24	6	AX111724	AX111724 Sequence	c 635	10.4	45.2	33	6	AR064935	AR064935 Sequence
c 563	10.4	45.2	24	6	AX289430	AX289430 Sequence	c 636	10.4	45.2	33	6	AR097146	AR097146 Sequence
c 564	10.4	45.2	24	6	AX290052	AX290052 Sequence	c 637	10.4	45.2	33	6	AR097188	AR097188 Sequence
c 565	10.4	45.2	24	6	AX292681	AX292681 Sequence	c 638	10.4	45.2	33	6	AR130644	AR130644 Sequence
c 566	10.4	45.2	24	6	E44016	E44016 Novel prote	c 639	10.4	45.2	33	6	AR130686	AR130686 Sequence
c 567	10.4	45.2	24	6	E59313	E59313 Method of r	c 640	10.4	45.2	33	6	AR171993	AR171993 Sequence
c 568	10.4	45.2	25	6	A87194	A87194 Sequence 5	c 641	10.4	45.2	33	6	AR172035	AR172035 Sequence
c 569	10.4	45.2	25	6	AX038338	AX038338 Sequence	c 642	10.4	45.2	33	6	BD006668	BD006668 Transport
c 570	10.4	45.2	25	6	AX279125	AX279125 Sequence	c 643	10.4	45.2	33	6	I82830	I82830 Sequence 9
c 571	10.4	45.2	25	6	AX350111	AX350111 Sequence	c 644	10.4	45.2	33	6	I82871	I82871 Sequence 50
c 572	10.4	45.2	25	6	I22153	I22153 Sequence 12	c 645	10.4	45.2	34	6	AR004298	AR004298 Sequence
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c 574	10.4	45.2	26	6	AR105759	AR105759 Sequence	c 647	10.4	45.2	34	6	AR085289	AR085289 Sequence
c 575	10.4	45.2	26	6	I14114	I14114 Sequence 28	c 648	10.4	45.2	34	6	AR095274	AR095274 Sequence
c 576	10.4	45.2	26	6	I22158	I22158 Sequence 17	c 649	10.4	45.2	34	6	AR153421	AR153421 Sequence
c 577	10.4	45.2	27	6	A02823	A02823 Artificial	c 650	10.4	45.2	34	6	AR178094	AR178094 Sequence
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c 579	10.4	45.2	27	6	A22669	A22669 Oligonucleo	c 652	10.4	45.2	34	6	AX247553	AX247553 Sequence
c 580	10.4	45.2	27	6	AX099274	AX099274 Sequence	c 653	10.4	45.2	34	6	I17720	I17720 Sequence 24
c 581	10.4	45.2	27	6	AX099275	AX099275 Sequence	c 654	10.4	45.2	34	6	I28968	I28968 Sequence 17
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c 583	10.4	45.2	27	6	AX349923	AX349923 Sequence	c 656	10.4	45.2	34	6	I38890	I38890 Sequence 17
c 584	10.4	45.2	27	6	E06044	E06044 Linker. 9/1	c 657	10.4	45.2	34	6	I69321	I69321 Sequence 6

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c 807	10.2	44.3	21	6	AR102141	AR102141 Sequence	c 880	10.2	44.3	31	6	AR118764	AR118764 Sequence
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c 812	10.2	44.3	21	6	I81264	I81264 Sequence 15	c 885	10.2	44.3	31	6	I32171	I32171 Sequence 46
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814	10.2	44.3	24	6	AR136099	AR136099 Sequence	c 887	10.2	44.3	31	6	I82467	I82467 Sequence 46
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c 816	10.2	44.3	24	6	AX288818	AX288818 Sequence	c 889	10.2	44.3	32	6	AR070736	AR070736 Sequence
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c 818	10.2	44.3	24	6	AX291184	AX291184 Sequence	c 891	10.2	44.3	32	6	AX181033	AX181033 Sequence
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c 823	10.2	44.3	24	6	I44524	I44524 Sequence 37	c 896	10.2	44.3	33	6	AR035445	AR035445 Sequence
824	10.2	44.3	25	6	AR109594	AR109594 Sequence	c 897	10.2	44.3	33	6	AR042999	AR042999 Sequence
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832	10.2	44.3	25	6	E27217	E27217 Novel physi	c 905	10.2	44.3	33	6	BD006095	BD006095 Feline po
833	10.2	44.3	25	6	E28275	E28275 Utilization	c 906	10.2	44.3	33	6	I62990	I62990 Sequence 11
834	10.2	44.3	25	6	E37241	E37241 Novel physi	c 907	10.2	44.3	33	6	I88743	I88743 Sequence 11
c 835	10.2	44.3	25	6	I68649	I68649 Sequence 14	c 908	10.2	44.3	34	6	A28098	A28098 Human GABA
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838	10.2	44.3	26	6	AR003516	AR003516 Sequence	c 911	10.2	44.3	34	6	AR148589	AR148589 Sequence
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c 843	10.2	44.3	27	6	A76892	A76892 Sequence 24	c 916	10.2	44.3	35	6	AX151753	AX151753 Sequence
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c 845	10.2	44.3	27	6	AR143859	AR143859 Sequence	c 918	10.2	44.3	36	6	AR137779	AR137779 Sequence
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c 847	10.2	44.3	27	6	AX192047	AX192047 Sequence	c 920	10.2	44.3	36	6	AX306753	AX306753 Sequence
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c 853	10.2	44.3	27	6	E35726	E35726 Toxoplasma	c 926	10.2	44.3	37	6	AR003506	AR003506 Sequence
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c 855	10.2	44.3	28	6	AR035817	AR035817 Sequence	c 928	10.2	44.3	37	6	AX080627	AX080627 Sequence
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c 865	10.2	44.3	29	6	BD007256	BD007256 Novel flt	c 938	10.2	44.3	38	6	E35663	E35663 Detection o
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c 867	10.2	44.3	30	6	AR083374	AR083374 Sequence	c 940	10.2	44.3	38	6	I26932	I26932 Sequence 2
c 868	10.2	44.3	30	6	AR085806	AR085806 Sequence	c 941	10.2	44.3	38	6	I76164	I76164 Sequence 8
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c 874	10.2	44.3	30	6	AX349406	AX349406 Sequence	c 947	10.2	44.3	39	6	AR086368	AR086368 Sequence
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c 876	10.2	44.3	31	6	AR016758	AR016758 Sequence	c 949	10.2	44.3	40	6	A63881	A63881 Sequence 6

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986 10.2 44.3 44 6 AR103982
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989 10.2 44.3 45 6 A05114
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997 10.2 44.3 46 6 AR087647
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A97298 Sequence 15
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ALIGNMENTS

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AX009578
LOCUS AX009578 23 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 3 from Patent WO9961607.
ACCESSION AX009578
VERSION AX009578.1 GI:9996816
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 23)
AUTHORS Dainert,I., Boehle,A., Gerdes,J. and Flad,H.D.
TITLE Antisense oligonucleotides for treating proliferating cells
JOURNAL Patent: WO 9961607-A 3 02-DEC-1999;
DEINERT IRINA (DE); BOEHLE ANDREAS (DE); GERDES JOHANNES (DE); FLAD
HANS DIETER (DE); FORSCHUNGSZENTRUM BORSTEL ZENT (DE)
FEATURES
Location/Qualifiers
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/db_xref="taxon:32630"
/note="Synthetisches Oligonukleotid"
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Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 accaggcgctctcggtggccacat 23
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Db 1 ACCAGGCGTCTCGTGGCCACAT 23
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AR044526
LOCUS AR044526 23 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 66 from patent US 5817495.
ACCESSION AR044526
VERSION AR044526.1 GI:5965991
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 23)
AUTHORS Pedersen,A.Hjelholt., Vind,J., Svendsen,A., Cherry,J.R., Lamsa,M.,
Schneider,P. and Jensen,B.Rostgaard.
TITLE H.sub.2 O.sub.2 -stable peroxidase variants
JOURNAL Patent: US 5817495-A 66 06-OCT-1998;
FEATURES
Location/Qualifiers
source 1. .23
/organism="unknown"
BASE COUNT 6 a 7 c 6 g 4 t
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Best Local Similarity 81.0%; Pred. No. 1.2e+04;
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RESULT 3
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LOCUS AX350362 37 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 18 from Patent WO0202765.
ACCESSION AX350362
VERSION AX350362.1 GI:18616024
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
REFERENCE 1 (sites)
AUTHORS Ribault,S., Neuville,P. and Mehtali,M.
TITLE Chimeric promoters for controlling expression in smooth muscle
JOURNAL Patent: WO 0202765-A 18 10-JAN-2002;
FEATURES
Location/Qualifiers
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Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 ccaggcgtctcgtgggccca 20
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Db 4 CCAAGCTTCTCGAGGCCA 22

RESULT 4
I25110/c I25110 34 bp DNA linear PAT 07-OCT-1996
LOCUS DEFINITION Sequence 16 from patent US 5547868.
ACCESSION I25110
VERSION I25110.1 GI:1604980
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 34)
AUTHORS Miller,W.L., Harikrishna,J.A. and Black,S.M.
TITLE Cholesterol disposal fusion enzymes
JOURNAL Patent: US 5547868-A 16 20-AUG-1996;
FEATURES Location/Qualifiers
source
1..34
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BASE COUNT 4 a 10 c 16 g 4 t
ORIGIN

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Best Local Similarity 88.2%; Pred. No. 2.9e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 gcgtctcgtgggccca 22
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Db 32 GCGCCTCCTGGGCCA 16

RESULT 5
AR058898/c AR058898 20 bp DNA linear PAT 29-SEP-1999
LOCUS DEFINITION Sequence 4 from patent US 5837836.
ACCESSION AR058898
VERSION AR058898.1 GI:5984475
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Friderici,K., Jones,M.Z., Chen,H. and Cavanagh,K.T.
TITLE Bovine beta-mannosidase nucleic acid sequence
JOURNAL Patent: US 5837836-A 4 17-NOV-1998;
FEATURES Location/Qualifiers
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/organism="unknown"
BASE COUNT 7 a 5 c 5 g 3 t
ORIGIN

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Best Local Similarity 80.0%; Pred. No. 3.6e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 aggcgtctcgtgggccacat 23
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Db 20 AGGTGCTCGTTAGCCACTT 1

RESULT 6
I36259/c I36259 20 bp DNA linear PAT 13-MAY-1997
LOCUS DEFINITION Sequence 4 from patent US 5605797.

ACCESSION I36259
VERSION I36259.1 GI:2086772
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Friderici,K., Jones,M.Z., Chen,H. and Cavanagh,K.T.
TITLE Bovine beta-mannosidase gene and methods of use
JOURNAL Patent: US 5605797-A 4 25-FEB-1997;
FEATURES Location/Qualifiers
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BASE COUNT 7 a 5 c 5 g 3 t
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Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Db 20 AGGTGCTCGTTAGCCACTT 1

RESULT 7
A27934 A27934 45 bp DNA linear PAT 27-JUN-1995
LOCUS DEFINITION Reshaped VI CDR-2 primer.
ACCESSION A27934
VERSION A27934.1 GI:1248522
KEYWORDS
SOURCE Synthetic construct.
ORGANISM Synthetic construct.
REFERENCE 1 (bases 1 to 45)
AUTHORS
TITLE HUMANIZED AND CHIMERIC MONOCLONAL ANTIBODIES
JOURNAL Patent: WO 9215683-A 23 17-SEP-1992;
FEATURES Location/Qualifiers
source
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/organism="synthetic construct"
/db_xref="taxon:32630"
BASE COUNT 9 a 15 c 10 g 11 t
ORIGIN

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Best Local Similarity 80.0%; Pred. No. 3.6e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 accaggcgtctcgtgggccca 20
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Db 23 ACCTGCTTCTGTGTGCCA 42

RESULT 8
AR050879 AR050879 45 bp DNA linear PAT 29-SEP-1999
LOCUS DEFINITION Sequence 33 from patent US 5830470.
ACCESSION AR050879
VERSION AR050879.1 GI:5974243
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 45)
AUTHORS Nakamura,K., Koike,M., Shitara,K., Hanai,N., Kuwana,Y. and
Hasegawa,M.
TITLE Humanized antibodies to ganglioside GM.sub.2
JOURNAL Patent: US 5830470-A 33 03-NOV-1998;
FEATURES Location/Qualifiers

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BASE COUNT 9 a 14 c 9 g 13 t
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Best Local Similarity 80.0%; Pred. No. 3.6e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Db 25 ACCTGGCTTCTGGTGGCCA 44

RESULT 9
LOCUS I26287 45 bp DNA linear PAT 07-OCT-1996
DEFINITION Sequence 36 from patent US 5558864.
ACCESSION I26287
VERSION I26287.1 GI:1606157
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 45)
AUTHORS Bendig,M.M., Kettleborough,C.A. and Saldanha,J.
TITLE Humanized and chimeric anti-epidermal growth factor receptor
JOURNAL Monoclonal antibodies
PATENT: US 5558864-A 36 24-SEP-1996;
FEATURES Location/Qualifiers
source 1. .45
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BASE COUNT 9 a 15 c 10 g 11 t
ORIGIN

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Best Local Similarity 80.0%; Pred. No. 3.6e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 accaggcgtctcgtggccca 20
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Db 23 ACCTGGCTTCTGGTGGCCA 42

RESULT 10
I51659/c I51659 45 bp DNA linear PAT 07-OCT-1997
LOCUS I51659
DEFINITION Sequence 6 from patent US 5645817.
ACCESSION I51659
VERSION I51659.1 GI:2472860
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 45)
AUTHORS Seemann,G. and Bosslet,K.
TITLE Granulocyte-binding antibody constructs, their preparation and use
JOURNAL Patent: US 5645817-A 6 08-JUL-1997;
FEATURES Location/Qualifiers
source 1. .45
/organism="unknown"
BASE COUNT 11 a 10 c 16 g 8 t
ORIGIN

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Best Local Similarity 80.0%; Pred. No. 3.6e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 accaggcgtctcgtggccca 20
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Db 1 accaggcgtctcgtggccca 20
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Db 23 ACCTGGCTTCTGGTGGCCA 4

RESULT 11
A57109 42 bp DNA linear PAT 03-MAR-1998
LOCUS A57109
DEFINITION Sequence 5 from Patent WO9630507.
ACCESSION A57109
VERSION A57109.1 GI:3713089
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 42)
AUTHORS Goding,C.R., White,M., Yavuzer,B.U. and Hurd,D.
TITLE VECTORS FOR DIFFERENTIAL EXPRESSION
JOURNAL Patent: WO 9630507-A 5 03-OCT-1996;
AMERSHAM INT PLC (GB)
FEATURES Location/Qualifiers
source 1. .42
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BASE COUNT 12 a 10 c 11 g 9 t
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Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 accaggcgtctcgtggccacat 23
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Db 9 AGCATGCATCTAGAGGCGCCGAT 31

RESULT 12
AX159478 50 bp DNA linear PAT 22-JUN-2001
LOCUS AX159478
DEFINITION Sequence 2806 from Patent WO0140521.
ACCESSION AX159478
VERSION AX159478.1 GI:14540809
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 50)
AUTHORS Shimkets,R.A. and Leach,M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0140521-A 2806 07-JUN-2001;
Curagen Corporation (US)
FEATURES Location/Qualifiers
source 1. .50
/organism="Homo sapiens"
/db_xref="taxon:9606"
misc_feature 25. .26
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misc_feature 26
Accession number cg42500135"
BASE COUNT 5 a 13 c 23 g 9 t
ORIGIN

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Best Local Similarity 83.3%; Pred. No. 5.7e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 caggcgtctcgtggccca 20
   ||| ||| ||| ||| ||| |||
Db 2 CACGTGTCTGTGGGCCA 19
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Query Match          56.5%; Score 13; DB 6; Length 29;
Best Local Similarity 76.2%; Pred. NO. 7.2e+04;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 17, 2002, 22:20:00 ; Search time 209.43 Seconds
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Searched: 1736436 seqs, 858457221 residues

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	ID	Description
1	23	100.0	23 21	Human cell cycle p
c 2	23	100.0	23 21	Human cell cycle p
3	14.6	63.5	48 15	Human beta-glucuro
c 4	14.2	61.7	30 20	PCR primer of the
5	14	60.9	50 22	Human SNP oligonuc
c 6	14	60.9	50 22	Human SNP oligonuc
c 7	13.8	60.0	34 16	Adrenodoxin-reduct
c 8	13.8	60.0	47 21	Human map-related
9	13.8	60.0	48 15	E.coli beta-glucur

Primer for amplify	15	AAQ78241	48	15	AAQ78241
Bovine beta-mannos	20	AAQ62433	20	18	AAQ62433
Bovine beta-mannos	20	AAV64130	20	18	AAV64130
REI human Ab L cha	45	AAQ63451	45	15	AAQ63451
Synthetic DNA for	45	AAQ9493	45	20	AAQ9493
Human Borna disease	27	AAV32874	27	19	AAV32874
CYC terminator pri	42	AAQ39606	42	17	AAQ39606
Human silent SNP c	50	AAI75865	50	22	AAI75865
CHO MEK gene PCR p	25	AAQ75369	25	22	AAQ75369
Growth hormone fam	41	AAI65184	41	22	AAI65184
Growth hormone fam	41	AAI65185	41	22	AAI65185
Exemplary DNA #6 e	42	AAA65068	42	21	AAA65068
Exemplary DNA #7 e	42	AAA65069	42	21	AAA65069
Human SNP oligonuc	50	AAI30289	50	22	AAI30289
Relaxin/IGF/insuli	24	ABA03536	24	24	ABA03536
M tuberculosis lys	31	AAQ56597	31	22	AAQ56597
Human map-related	47	AAQ66679	47	21	AAQ66679
Human polymorphic	21	AAZ25868	21	19	AAZ25868
Oligonucleotide 10	27	AAV66554	27	19	AAV66554
Human beta-globin	27	AAA38490	27	19	AAA38490
V. cholerae thyA g	27	AAZ40651	27	21	AAZ40651
Primer CTW2 for Fa	28	AAQ88886	28	18	AAQ88886
Human Fas antigen	28	AAV70124	28	19	AAV70124
Mouse IL-3 recepto	28	AAA72113	28	21	AAA72113
Human Fas antigen	34	AAA11551	34	21	AAA11551
Primer for coding	34	AAV08045	34	19	AAV08045
Humanised antibody	41	AAV26397	41	19	AAV26397
Humanised antibody	41	AAV21675	41	19	AAV21675
Human silent SNP c	50	AAI75839	50	22	AAI75839
Strand 1 of DX (do	25	AAI10689	25	22	AAI10689
Camel binder IDBOV	29	AAQ57490	29	22	AAQ57490
Camel binder IDBOV	29	AAQ57492	29	22	AAQ57492
MHC class I allele	31	AAQ85848	31	16	AAQ85848
MHC CW3 amplifcat	31	AAQ85778	31	16	AAQ85778
MHC CW3 cDNA nts 1	31	AAQ85742	31	16	AAQ85742
Human p53 gene pri	37	AAQ90420	37	20	AAQ90420
Shiga-like toxin 1	40	AAQ63106	40	21	AAQ63106
Shiga-like toxin 1	42	AAQ63105	42	21	AAQ63105
Shiga-like toxin 1	42	AAQ63104	42	21	AAQ63104
Erwinia herbicola	44	AAQ87548	44	20	AAQ87548
Oligonucleotide Cr	44	AAQ62586	44	22	AAQ62586
Human SNP oligonuc	50	AAI34518	50	22	AAI34518
Human SNP oligonuc	50	AAI34573	50	22	AAI34573
Human oligonucleot	50	AAQ09047	50	22	AAQ09047
Capture oligonucle	20	AAI95090	20	24	AAI95090
Human collagen COL	23	AAQ22420	23	22	AAQ22420
Capture oligonucle	24	AB186750	24	24	AB186750
Capture oligonucle	24	AB186751	24	24	AB186751
Neisseria species	26	AAI254898	26	21	AAI254898
SAR element PCR pr	31	AAQ43374	31	18	AAQ43374
Neisseria gonorrhoe	38	AAQ56345	38	20	AAQ56345
WO 990191 SeqID #	46	AAQ26503	46	20	AAQ26503
Human PECAM-1 anti	20	AAQ08885	20	20	AAQ08885
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A. utahensis ECB d	22	AAV62031	22	19	AAV62031
c-kit mRNA antisen	24	AAQ30865	24	13	AAQ30865
Antisense oligonuc	24	AAQ37317	24	13	AAQ37317
c-kit mRNA antisen	25	AAQ30864	25	13	AAQ30864
c-kit mRNA antisen	26	AAQ30863	26	13	AAQ30863
Antisense oligonuc	26	AAQ37315	26	13	AAQ37315
Polymorphic fragme	29	AAQ40005	29	21	AAQ40005
Human single nucle	31	AAI29754	31	22	AAI29754
Human short chain	33	AAI99823	33	24	AAI99823
B. megaterium BM-3	34	AAQ26266	34	22	AAQ26266
B. megaterium BM-3	34	AAQ26267	34	22	AAQ26267
Antisense probe DM	37	AAQ98445	37	16	AAQ98445
Oligonucleotide DM	37	AAQ24984	37	20	AAQ24984
c-kit mRNA antisen	40	AAQ30862	40	13	AAQ30862
Human c-kit fragme	40	AAQ37327	40	21	AAQ37327
Exemplary DNA #1	42	AAQ5063	42	21	AAQ5063
Exemplary DNA #9 e	42	AAQ65071	42	21	AAQ65071
Catalytic DNA, met	47	AAQ48616	47	18	AAQ48616
Human map-related	47	AAQ67343	47	21	AAQ67343

83	11.8	51.3	20	22	AAK94980	Human cDNA clone-s	156	11.6	50.4	41	19	AAV41677	Glucose-Inducible
c 84	11.8	51.3	22	24	AAAD24620	Trichoderma reesei	157	11.6	50.4	43	12	AAQ12253	HIV-1 LTR mutation
c 85	11.8	51.3	24	21	AAA47675	RACE oligo d(T) an	158	11.6	50.4	43	22	AAQ09082	Human oligonucleot
c 86	11.8	51.3	24	21	AAA43425	Linker variant pol	159	11.6	50.4	48	17	AAT06971	DNA encoding GM-CS
c 87	11.8	51.3	24	21	AAA45931	Linker variant pol	160	11.6	50.4	50	18	AAT78670	Construction oligo
c 88	11.8	51.3	24	21	AAAS2843	DNA linker #5 for	161	11.6	50.4	50	22	AAL30342	Human SNP oligonuc
c 89	11.8	51.3	26	18	AAAS6069	Human cysteine pro	c 162	11.4	49.6	13	23	ABC51158	Oligonucleotide SE
c 90	11.8	51.3	29	22	AAAD18771	Primer Y2H-MCS2, t	c 163	11.4	49.6	13	23	ABC51159	Oligonucleotide SE
c 91	11.8	51.3	31	19	AAAV10524	Human ITAK cDNA li	c 164	11.4	49.6	13	23	ABC51180	Oligonucleotide SE
c 92	11.8	51.3	31	22	AAAH47094	B. napus cold indu	c 165	11.4	49.6	13	23	ABC51181	Oligonucleotide SE
c 93	11.8	51.3	31	22	AAAT29665	Human single nucle	c 166	11.4	49.6	17	20	AAH44577	Human MACHR-6 anti
c 94	11.8	51.3	31	22	AAI30503	Human single nucle	c 167	11.4	49.6	17	20	AAH44577	Human flh84g5 3' u
c 95	11.8	51.3	32	20	AAAX19726	Human AIM-1 PCR pr	c 168	11.4	49.6	17	20	AAH44577	Human MACHR-6 cDNA
c 96	11.8	51.3	37	22	AAH24148	Human E2F-1 promot	c 169	11.4	49.6	19	21	AAH83539	cdk-we-hu ribozyme
c 97	11.8	51.3	39	19	AAV624466	Oligo-dT-anchor pr	c 170	11.4	49.6	19	22	AAH58701	Cdk-we-hu ribozyme
c 98	11.8	51.3	39	19	AAV60309	Oligo-dT anchor pr	c 171	11.4	49.6	21	22	AAH58701	Human gene single
c 99	11.8	51.3	39	20	AAAS2554	Anchor tailed prim	c 172	11.4	49.6	22	19	AAV45543	PCR anchor primer.
c 100	11.8	51.3	39	20	AAAS2559	Anchor tailed prim	c 173	11.4	49.6	22	19	AAV60310	PCR anchor primer.
c 101	11.8	51.3	39	20	AAAX81830	PCR primer used to	c 174	11.4	49.6	22	20	AAZ32556	Anchor primer, for
c 102	11.8	51.3	39	21	AAAX81836	PCR primer used to	c 175	11.4	49.6	22	20	AAZ32556	Anchor primer, for
c 103	11.8	51.3	39	21	AAAS0155	Oligo dT-anchor pr	c 176	11.4	49.6	22	20	AAZ32556	Anchor primer, for
c 104	11.8	51.3	39	22	AAH48707	T. thermophila tri	c 177	11.4	49.6	22	20	AAZ36784	PCR primer for hum
c 105	11.8	51.3	39	22	AAAD12539	5' sense PCR prime	c 178	11.4	49.6	22	20	AAZ36784	PCR primer AP used
c 106	11.8	51.3	39	22	AAAC85686	Oligo-dT anchor pr	c 179	11.4	49.6	22	21	AAZ27900	GEF containing NEK
c 107	11.8	51.3	39	24	AAAS16497	Anchored RACE prim	c 180	11.4	49.6	22	21	AAZ27900	PCR anchor primer
c 108	11.8	51.3	40	20	AAAS26998	Human chromosome 1	c 181	11.4	49.6	22	21	AAZ27900	5' sense anchor PC
c 109	11.8	51.3	40	22	AAAS07185	Oligo-(T) adaptor	c 182	11.4	49.6	22	22	AAZ12530	Primer used to amp
c 110	11.8	51.3	40	22	AAAF61931	T. thermophila del	c 183	11.4	49.6	22	22	AAH42284	Anchor primer, for
c 111	11.8	51.3	40	22	AAAF24483	Human ICE coding s	c 184	11.4	49.6	22	22	AAH42284	3'RACE anchor prim
c 112	11.8	51.3	41	22	AAAC87377	Staphylococcus aur	c 185	11.4	49.6	22	24	AAH42284	Marmoset Type II G
c 113	11.8	51.3	41	21	AAA38054	Linker used in RGC	c 186	11.4	49.6	22	24	AAH42284	Capture oligonucle
c 114	11.8	51.3	42	14	AAO53703	Nucleic acid ligase	c 187	11.4	49.6	24	24	ABT89857	Capture oligonucle
c 115	11.8	51.3	42	17	AAOT07833	HIV-1 RT-SELEX ide	c 188	11.4	49.6	24	24	ABT89857	Fused androgen rec
c 116	11.8	51.3	42	18	AAV00918	SELEX ligand 2.20	c 189	11.4	49.6	25	22	AAH42284	Alzheimer's diseas
c 117	11.8	51.3	42	19	AAV14703	Isolate 2.20 of SE	c 190	11.4	49.6	27	19	AAV24334	Primer #10 for con
c 118	11.8	51.3	42	20	AAV759778	RNA ligand sequenc	c 191	11.4	49.6	27	21	AAZ63466	Hammerhead ribozym
c 119	11.8	51.3	42	21	AAAS92878	High-affinity nucl	c 192	11.4	49.6	27	22	AAAF27235	Pseudomonas aerugi
c 120	11.8	51.3	45	22	AAI74714	Human silent SNP c	c 193	11.4	49.6	27	24	AAAS16958	Human L-selectin s
c 121	11.8	51.3	45	22	AAI74715	Human silent SNP c	c 194	11.4	49.6	28	20	AAO36004	PCR primer MutII u
c 122	11.8	51.3	47	21	AAI74715	Human map-related	c 195	11.4	49.6	28	22	AAH42292	Primer used to mut
c 123	11.8	51.3	50	22	AAI32055	Human SNP oligonuc	c 196	11.4	49.6	28	22	AAH42292	Primer used to amp
c 124	11.8	51.3	50	22	AAI32056	Human SNP oligonuc	c 197	11.4	49.6	28	20	AAH42292	Mouse Al T cell re
c 125	11.6	50.4	18	21	AAAS2513	Antisense oligonuc	c 198	11.4	49.6	29	21	AAO40056	Polymorphic fragme
c 126	11.6	50.4	20	21	AAH48260	Oligonucleotide #	c 199	11.4	49.6	29	21	AAZ24184	Human BRCA2 primer
c 127	11.6	50.4	20	24	AB195780	Capture oligonucle	c 200	11.4	49.6	29	22	AAI12944	Rainbow trout prep
c 128	11.6	50.4	20	24	AB197468	Capture oligonucle	c 201	11.4	49.6	30	16	AAQ90548	Proximal flanking
c 129	11.6	50.4	22	18	AAV70104	Primer for ostrich	c 202	11.4	49.6	30	16	AAQ90548	Proximal flanking
c 130	11.6	50.4	22	19	AAV52977	Mouse CASH homolog	c 203	11.4	49.6	30	16	AAQ82998	DNA/RNA chimeric p
c 131	11.6	50.4	22	19	AAV28306	Ostrich alpha-subu	c 204	11.4	49.6	30	16	AAQ82998	DNA/RNA chimeric p
c 132	11.6	50.4	23	22	AAAS22049	Human COL1A1 PCR p	c 205	11.4	49.6	30	18	AAAT97981	Proximal flanking
c 133	11.6	50.4	24	24	AB188130	Capture oligonucle	c 206	11.4	49.6	30	18	AAAT97982	Target to proximal
c 134	11.6	50.4	24	24	AB188131	Capture oligonucle	c 207	11.4	49.6	30	19	AAV54229	Primer KCl118 used
c 135	11.6	50.4	24	24	AB191506	Capture oligonucle	c 208	11.4	49.6	30	19	AAV33321	Anti-CD23 6G5 anti
c 136	11.6	50.4	24	24	AB191507	Capture oligonucle	c 209	11.4	49.6	30	19	AAV33321	Human presenilin 2
c 137	11.6	50.4	27	24	ABK16698	p53 primer Msp-O-4	c 210	11.4	49.6	30	19	AAV39442	Human presenilin 2
c 138	11.6	50.4	28	18	AAV76430	Human endothelin B	c 211	11.4	49.6	30	19	AAV16255	Proximal flanking
c 139	11.6	50.4	28	20	AAAS4221	Endothelin recepto	c 212	11.4	49.6	30	19	AAV16255	Proximal flanking
c 140	11.6	50.4	28	21	AAAF19787	Endothelin ETA rec	c 213	11.4	49.6	30	20	AAAS5311	Soluble sc-rCR fus
c 141	11.6	50.4	28	21	AAAS33665	Low adenosine anti	c 214	11.4	49.6	30	21	AAH40405	Human hDRC6 exon 3
c 142	11.6	50.4	29	21	AAAS60978	Oligonucleotide PC	c 215	11.4	49.6	32	18	AAQ03582	Preprochymosin lea
c 143	11.6	50.4	30	18	AAV02781	Target binding seq	c 216	11.4	49.6	32	18	AAQ03582	Blocking oligonucle
c 144	11.6	50.4	31	16	AAV45064	HCW pp28-luc prom	c 217	11.4	49.6	32	21	AAAS1695	Sin5122F primer fo
c 145	11.6	50.4	33	13	AAQ31170	21-hydroxylase fra	c 218	11.4	49.6	33	20	AAH55438	Soluble sc-TCR fus
c 146	11.6	50.4	33	13	AAQ46476	Probe l39 for geno	c 219	11.4	49.6	33	21	AAZ44684	Human hemoglobin b
c 147	11.6	50.4	33	23	AB197717	Hepatitis C virus	c 220	11.4	49.6	33	22	AAAF26335	B. megaterium BM-3
c 148	11.6	50.4	33	23	AB197722	Endogenous human G	c 221	11.4	49.6	33	22	AAAF26335	B. megaterium BM-3
c 149	11.6	50.4	37	18	AAQ91802	Target binding seq	c 222	11.4	49.6	35	20	AAAS36573	PCR primer for hum
c 150	11.6	50.4	38	14	AAO48371	25D2 MAb heavy cha	c 223	11.4	49.6	35	22	AAAS00262	LPA receptor-relat
c 151	11.6	50.4	38	14	AAQ48059	Human gamma4 const	c 224	11.4	49.6	36	17	AAAT41885	Human beta-globin
c 152	11.6	50.4	38	16	AAQ98878	Humanised antibody	c 225	11.4	49.6	36	18	AAAT76077	Human FC-epsilon r
c 153	11.6	50.4	39	12	AAQ11091	Globin beta A B-13	c 226	11.4	49.6	36	20	AAH53876	Human IgE receptor
c 154	11.6	50.4	39	21	AAAI12124	T. brucei trypanos	c 227	11.4	49.6	36	21	AAAF19441	Human IgE receptor
c 155	11.6	50.4	40	16	AAH89092	Elastase DNA nucle	c 228	11.4	49.6	36	21	AAAF69961	TGF-beta-1-binding

c 229	11.4	49.6	36	21	AAA33319	Low adenosine anti	302	11.2	48.7	24	24	AB186364	Capture oligonucle
c 230	11.4	49.6	36	21	AAA35845	Pemrutein linked e	c 303	11.2	48.7	24	24	AB186365	Capture oligonucle
c 231	11.4	49.6	38	20	AA232559	Anchor tailed prim	c 304	11.2	48.7	24	24	AB192244	Capture oligonucle
c 232	11.4	49.6	38	20	AA232564	Anchor tailed prim	c 305	11.2	48.7	24	24	AB192245	Capture oligonucle
c 233	11.4	49.6	38	20	AA245535	Tumour-specific Ig	c 306	11.2	48.7	25	20	AA221480	Primer #1 for fusi
c 234	11.4	49.6	39	20	AA244492	CC49/218 SCA (sing	c 307	11.2	48.7	26	21	AA240042	PCR primer MO10BAC
c 235	11.4	49.6	40	21	AA296092	Polynucleotide seq	c 308	11.2	48.7	27	20	AA240042	Human beta-1,4-gal
c 236	11.4	49.6	41	21	AAA09067	Primer for human h	c 309	11.2	48.7	27	20	AA240042	Human cancer anti
c 237	11.4	49.6	41	22	AA170160	Human uroplakin Ia	c 310	11.2	48.7	27	21	AA258602	PCR primer hGT-6Sp
c 238	11.4	49.6	41	22	AA262364	PCR primer used to	c 311	11.2	48.7	28	21	AA258602	Rapamycin rapc gen
c 239	11.4	49.6	42	22	AAH91968	Human inflammatory	c 312	11.2	48.7	29	20	AAA19923	Integrin alpha 6 s
c 240	11.4	49.6	44	15	AAQ78507	Human GRP78 Not1-1	c 313	11.2	48.7	29	20	AA222170	Integrin subunit b
c 241	11.4	49.6	44	20	AAH81811	Primer used to amp	c 314	11.2	48.7	29	21	AA222170	Hammerhead ribozym
c 242	11.4	49.6	45	13	AAQ27685	FGB2 RNA for an ep	c 315	11.2	48.7	29	21	AA222170	Hammerhead ribozym
c 243	11.4	49.6	45	13	AAQ27689	FGB2 RNA for an ep	c 316	11.2	48.7	29	21	AA222170	Hammerhead ribozym
c 244	11.4	49.6	45	22	AA27689	Mutagenic PCR prim	c 317	11.2	48.7	29	21	AA222170	Hammerhead ribozym
c 245	11.4	49.6	45	22	AA27689	Mutagenic PCR prim	c 318	11.2	48.7	29	21	AA222170	Alphavirus synthes
c 246	11.4	49.6	45	22	AA27689	Mutagenic PCR prim	c 319	11.2	48.7	29	21	AA222170	Oestrogen receptor
c 247	11.4	49.6	45	22	AAH79093	Human insulin homo	c 320	11.2	48.7	29	24	AA225115	Sindbis virus cDNA
c 248	11.4	49.6	45	22	AA274532	Human MKK3 site-di	c 321	11.2	48.7	30	22	AA258601	Human cancer anti
c 249	11.4	49.6	45	22	AA274533	Human MKK3 site-di	c 322	11.2	48.7	30	22	AA258601	Bacterial 23S/5S R
c 250	11.4	49.6	45	22	AA264157	Human MKK mutageni	c 323	11.2	48.7	30	22	AA258601	Bacterial 23S/5S R
c 251	11.4	49.6	47	21	AA267973	Human map-related	c 324	11.2	48.7	30	22	AA258601	Rainbow trout prep
c 252	11.4	49.6	47	21	AA269020	Human map-related	c 325	11.2	48.7	31	21	AA237405	PCR primer for hum
c 253	11.4	49.6	47	21	AA269080	Human map-related	c 326	11.2	48.7	31	22	AA237405	Human single nucle
c 254	11.4	49.6	48	12	AAQ14775	Rennin gene probe.	c 327	11.2	48.7	31	22	AA237405	Human DKK epsilon
c 255	11.4	49.6	48	13	AAQ27686	FGB2 RNA for an ep	c 328	11.2	48.7	36	19	AA258601	Anti-human Fas hum
c 256	11.4	49.6	48	13	AAQ27687	FGB2 RNA for an ep	c 329	11.2	48.7	36	19	AA258601	Humanised anti-Fas
c 257	11.4	49.6	48	13	AAQ27690	FGB2 RNA for an ep	c 330	11.2	48.7	38	20	AA258601	Oligonucleotide us
c 258	11.4	49.6	48	13	AAQ27691	FGB2 RNA for an ep	c 331	11.2	48.7	39	16	AAQ89094	Elastase DNA nucle
c 259	11.4	49.6	49	20	AA231116	RNA ligand to hTGF	c 332	11.2	48.7	39	16	AAQ89116	Elastase DNA nucle
c 260	11.4	49.6	50	22	AA229212	Human SNP oligonuc	c 333	11.2	48.7	40	14	AAQ1768	Myc EMSA probe pro
c 261	11.4	49.6	50	22	AA231279	Human SNP oligonuc	c 334	11.2	48.7	40	16	AAQ89110	Elastase DNA nucle
c 262	11.4	49.6	50	22	AA231354	Human SNP oligonuc	c 335	11.2	48.7	40	16	AAQ89115	Elastase DNA nucle
c 263	11.4	49.6	50	22	AA233627	Human SNP oligonuc	c 336	11.2	48.7	40	17	AA258601	Fibrin clot bindin
c 264	11.4	49.6	50	22	AA233628	Human SNP oligonuc	c 337	11.2	48.7	40	19	AA258601	Maize polymorphic
c 265	11.4	49.6	50	22	AA233628	Human SNP oligonuc	c 338	11.2	48.7	40	20	AA228137	PCR primer for hum
c 266	11.4	49.6	50	22	AA233628	Human silent SNP c	c 339	11.2	48.7	40	20	AA228137	PCR primer for hum
c 267	11.4	49.6	50	22	AA267796	Crosslinking probe	c 340	11.2	48.7	40	22	AA228137	Human follistatin-
c 268	11.4	49.6	50	23	ABL01021	Human SNP involvin	c 341	11.2	48.7	40	22	AA228137	Human follistatin-
c 269	11.2	48.7	16	18	AA268901	Human BCR exon 11	c 342	11.2	48.7	41	19	AA258601	Maize polymorphic
c 270	11.2	48.7	17	20	AA220387	Integrin alpha 6 s	c 343	11.2	48.7	42	24	AA258601	Pseudomonas carbox
c 271	11.2	48.7	17	21	AA202620	Hammerhead ribozym	c 344	11.2	48.7	42	24	AA258601	Primer FKBP5fil-A
c 272	11.2	48.7	18	19	AA247173	PCR primer used to	c 345	11.2	48.7	43	19	AA258601	Yeast PCR primer F
c 273	11.2	48.7	18	19	AA247173	PCR primer used to	c 346	11.2	48.7	43	21	AA258601	FKBP gene PCR prim
c 274	11.2	48.7	18	21	AA263098	Human cellular pro	c 347	11.2	48.7	43	21	AA258601	Adaptor #3 used in
c 275	11.2	48.7	18	21	AA263100	Human cellular pro	c 348	11.2	48.7	43	21	AA258601	Reverse PCR primer
c 276	11.2	48.7	18	21	AA263557	Antisense oligonuc	c 349	11.2	48.7	43	21	AA258601	Human map-related
c 277	11.2	48.7	18	21	AA263557	Antisense oligonuc	c 350	11.2	48.7	43	21	AA258601	Human map-related
c 278	11.2	48.7	18	21	AA263557	Antisense oligonuc	c 351	11.2	48.7	47	21	AA258601	Human map-related
c 279	11.2	48.7	18	21	AA243282	Murine Sox2 gene P	c 352	11.2	48.7	47	18	AA258601	Multiple cloning s
c 280	11.2	48.7	19	21	AA258670	Nucleotide sequenc	c 353	11.2	48.7	49	18	AA258601	Detection probe SE
c 281	11.2	48.7	19	21	AA258672	Nucleotide sequenc	c 354	11.2	48.7	50	19	AA258601	Human SNP oligonuc
c 282	11.2	48.7	19	21	AA258672	Nucleotide sequenc	c 355	11.2	48.7	50	22	AA228818	Human SNP oligonuc
c 283	11.2	48.7	19	21	AA258677	Nucleotide sequenc	c 356	11.2	48.7	50	22	AA229632	Human SNP oligonuc
c 284	11.2	48.7	19	21	AA258681	Nucleotide sequenc	c 357	11.2	48.7	50	22	AA229632	Human SNP oligonuc
c 285	11.2	48.7	19	21	AA258683	Nucleotide sequenc	c 358	11.2	48.7	50	22	AA229632	Human SNP oligonuc
c 286	11.2	48.7	20	20	AA231252	CCP5 gene inhibiti	c 359	11.2	48.7	50	22	AA229632	Human SNP oligonuc
c 287	11.2	48.7	20	21	AA263103	Human cellular pro	c 360	11.2	48.7	50	22	AA229632	Human SNP oligonuc
c 288	11.2	48.7	20	21	AA278367	Humanised anti-Fas	c 361	11	47.8	19	21	AA278367	Forward primer for
c 289	11.2	48.7	21	19	AA225900	Human polymorphic	c 362	11	47.8	20	16	AA278367	Primer B (Group 2,
c 290	11.2	48.7	21	20	AA225900	Plasmid pTNB110 co	c 363	11	47.8	20	16	AA278367	E. coli SecA antis
c 291	11.2	48.7	21	22	AAH00933	Trypanosomatidae d	c 364	11	47.8	20	22	AA278367	Human PARP-2 ant
c 292	11.2	48.7	22	18	AA288943	Bumper primer 3 fo	c 365	11	47.8	20	22	AA278367	Type-C natriuretic
c 293	11.2	48.7	23	20	AA234031	Human CDC28-#3 RNA	c 366	11	47.8	21	19	AA278367	Human polymorphic
c 294	11.2	48.7	23	20	AA234031	PCR primer B233 us	c 367	11	47.8	21	22	AA278367	Tumour antigen ant
c 295	11.2	48.7	23	20	AA278706	Human PRO615 rever	c 368	11	47.8	21	22	AA278706	Human gene single
c 296	11.2	48.7	23	21	AA278706	Human PRO615 rever	c 369	11	47.8	21	22	AA278706	Human gene single
c 297	11.2	48.7	23	21	AA258146	Primer nol4-3 used	c 370	11	47.8	22	19	AA278706	Human biallelic po
c 298	11.2	48.7	24	21	AA272580	PCR primer used to	c 371	11	47.8	22	19	AA272580	L-oncogene primer
c 299	11.2	48.7	24	21	AA272580	Capture oligonucle	c 372	11	47.8	23	13	AA272580	c-kit mRNA antisen
c 300	11.2	48.7	24	24	AB182978	Capture oligonucle	c 373	11	47.8	23	13	AA272580	Antisense oligonuc
c 301	11.2	48.7	24	24	AB182979	Capture oligonucle	c 374	11	47.8	24	19	AA272580	Primer 35S for her

375	11	47.8	26	16	AAQ89946	Listeria 16S rDNA	c 448	10.8	47.0	20	24	ABI96448	Capture oligonucle
376	11	47.8	26	18	AAQ22952	Human cathepsin Y	449	10.8	47.0	21	15	AAQ68443	Pseudomonas glutam
377	11	47.8	26	20	AAZ11424	Hypoxia responsive	450	10.8	47.0	21	19	AAQ26751	Human polymorphic
378	11	47.8	26	12	AAQ12009	Murine HRE DNA glu	451	10.8	47.0	21	22	AAQ63369	Forward PCR primer
c 379	11	47.8	27	11	AAQ14971	Beta A/S globin ge	c 452	10.8	47.0	23	17	AAQ10339	Anti-p. aeruginosa
380	11	47.8	27	14	AAQ35914	Human/monkey heavy	c 453	10.8	47.0	23	24	ABA04439	Human P1009 PCR p
381	11	47.8	27	15	AAQ56634	PCR primer for mou	454	10.8	47.0	24	14	AAQ46694	Beta-actin primer
382	11	47.8	27	18	AAQ95133	Human or monkey Ig	455	10.8	47.0	24	14	AAQ47685	Beta-actin PCR pri
383	11	47.8	27	18	AAQ92209	Monkey/human heavy	456	10.8	47.0	24	15	AAQ78130	Specific oligonucle
384	11	47.8	27	18	AAQ62880	Human or monkey VH	c 457	10.8	47.0	24	17	AAQ38351	G3PDH primer 2. S
385	11	47.8	27	19	AAV31393	Human or monkey he	c 458	10.8	47.0	24	18	AAQ70485	Dystrophin reverse
386	11	47.8	27	19	AAV23771	Primer for Anti-CD	c 459	10.8	47.0	24	19	AAV46349	PCR primer for ser
387	11	47.8	27	19	AAV05661	Human/monkey Vh4 1	c 460	10.8	47.0	24	19	AAV16411	Nucleotide sequenc
c 388	11	47.8	27	21	AAQ64489	Primer for triose	c 461	10.8	47.0	24	19	AAV16411	Primer used in pre
389	11	47.8	28	19	AAQ66672	Mouse interleukin-	c 462	10.8	47.0	24	20	AAQ23114	G3PDH specific 3'
390	11	47.8	28	21	AAQ78371	Fas antigen extrac	c 463	10.8	47.0	24	20	AAQ21558	3' PCR primer used
391	11	47.8	29	19	AAV42718	5' PCR primer used	c 464	10.8	47.0	24	20	AAQ21363	Prime HGA for G3PD
392	11	47.8	29	19	AAV23922	PCR primer for hum	c 465	10.8	47.0	24	20	AAQ01680	Human G3PDH PCR pr
c 393	11	47.8	29	22	AAQ99441	Immunostimulatory	c 466	10.8	47.0	24	21	AAQ96957	PCR primer used to
394	11	47.8	30	19	AAV44993	15D3 antibody heav	c 467	10.8	47.0	24	21	AAQ62449	Human G3PDH antisense
c 395	11	47.8	30	20	AAZ10945	15D3 VH chain CDR3	c 468	10.8	47.0	24	21	AAQ07402	PCR primer for gly
c 396	11	47.8	30	21	AAQ49127	1265MAS primer use	c 469	10.8	47.0	24	21	AAQ58346	Human GAPDH specif
c 397	11	47.8	30	21	AAQ52110	Maize CGEVL32RB_u	c 470	10.8	47.0	24	22	AAQ22599	Human G3PDH specif
c 398	11	47.8	30	21	AAQ52110	Primer CGEVL32RB_u	c 471	10.8	47.0	24	22	AAQ22460	GAPDH downstream a
399	11	47.8	32	19	AAV41678	Glucose-inducible	c 472	10.8	47.0	24	22	AAQ22468	GAPDH downstream a
c 400	11	47.8	32	20	AAQ17755	Oligo #23 for ampl	c 473	10.8	47.0	24	22	AAQ23652	Glyceraldehyde 3-p
c 401	11	47.8	32	21	AAQ30780	Human GPR32 (K255A	c 474	10.8	47.0	24	22	AAQ84204	G3PDH PCR primer.
c 402	11	47.8	32	21	AAQ30781	Human GPR32 (K255A	c 475	10.8	47.0	24	22	AAQ25091	PCR primer for M.
c 403	11	47.8	32	22	AAQ00349	PCR primer #3, use	c 476	10.8	47.0	24	22	AAQ89866	Human GAPDH cDNA r
c 404	11	47.8	33	13	AAQ31144	Probe 113 specific	c 477	10.8	47.0	24	24	ABA92499	Human G3PDH specif
c 405	11	47.8	33	14	AAQ46450	Hepatitis C virus	c 478	10.8	47.0	24	24	ABA05425	Human Hcsgk-1 PCR
c 406	11	47.8	33	20	AAQ17754	Oligo #24 for ampl	c 479	10.8	47.0	24	24	ABA96191	Human G3PDH PCR pr
c 407	11	47.8	33	21	AAQ00551	Enhanced yellow fl	c 480	10.8	47.0	24	24	ABI82576	Capture oligonucle
c 408	11	47.8	33	22	AAQ05932	EvFP-C1 reverse PC	c 481	10.8	47.0	24	24	ABI82577	Capture oligonucle
c 409	11	47.8	34	18	AAV02499	Human tyrosine pho	c 482	10.8	47.0	24	24	ABI84870	Capture oligonucle
c 410	11	47.8	36	18	AAQ67301	Islet cell antigen	c 483	10.8	47.0	24	24	ABI84871	Capture oligonucle
c 411	11	47.8	36	22	AAQ16693	Cucumis melo P1124	c 484	10.8	47.0	24	24	ABI84978	Capture oligonucle
c 412	11	47.8	36	22	AAQ55634	Primer for human e	c 485	10.8	47.0	24	24	ABI84979	Capture oligonucle
c 413	11	47.8	37	22	AAQ25105	PCR primer for M.	c 486	10.8	47.0	24	24	ABI87156	Capture oligonucle
c 414	11	47.8	39	24	ABA02832	Mycobacterium tube	c 487	10.8	47.0	24	24	ABI87157	Capture oligonucle
c 415	11	47.8	40	20	AAQ56318	Neisseria gonorrhoe	c 488	10.8	47.0	24	24	ABI88188	Capture oligonucle
c 416	11	47.8	40	21	AAQ96069	Polynucleotide seq	c 489	10.8	47.0	24	24	ABI88189	Capture oligonucle
c 417	11	47.8	40	22	AAQ18011	A. fumigatus codon	c 490	10.8	47.0	24	24	ABI89242	Capture oligonucle
c 418	11	47.8	40	22	AAQ166507	Rat SAPK interacti	c 491	10.8	47.0	24	24	ABI89243	Capture oligonucle
c 419	11	47.8	41	18	AAQ59260	Forward primer SIN	c 492	10.8	47.0	24	24	ABI89466	Capture oligonucle
c 420	11	47.8	41	20	AAQ58502	Forward primer SIN	c 493	10.8	47.0	24	24	ABI89467	Capture oligonucle
c 421	11	47.8	41	20	AAQ56317	Neisseria gonorrhoe	c 494	10.8	47.0	24	24	ABI89618	Capture oligonucle
c 422	11	47.8	42	21	AAQ87168	CaMV35S enhancer e	c 495	10.8	47.0	24	24	ABI89619	Capture oligonucle
c 423	11	47.8	45	19	AAQ26491	Human cytohesin-1	c 496	10.8	47.0	24	24	ABI91842	Capture oligonucle
c 424	11	47.8	45	19	AAQ26492	Human cytohesin-1	c 497	10.8	47.0	24	24	ABI91843	Capture oligonucle
c 425	11	47.8	45	20	AAQ02196	Human JEG62 PCR pr	c 498	10.8	47.0	24	24	ABI92772	Capture oligonucle
c 426	11	47.8	47	21	AAQ268926	Human map-related	c 499	10.8	47.0	24	24	ABI92773	Capture oligonucle
c 427	11	47.8	48	13	AAQ31373	IL-6R antibody pri	c 500	10.8	47.0	25	20	AAQ35971	Primer used to amp
c 428	11	47.8	48	15	AAQ56727	Sequence of oligo	c 501	10.8	47.0	25	21	AAQ87784	Rat SNORF36 recept
c 429	11	47.8	49	18	AAQ80483	Hepatoma AS-30D Ty	c 502	10.8	47.0	25	21	AAQ63752	Maize cytotype-spe
c 430	11	47.8	50	13	AAQ21752	HCV probe 42.L1A2C	c 503	10.8	47.0	25	21	AAQ62444	Human Akt-3 cDNA 3
c 431	11	47.8	50	21	AAQ77273	Human clone cq4398	504	10.8	47.0	26	19	AAQ08044	Primer for coding
c 432	11	47.8	50	22	AAQ29962	Human SNP oligonuc	505	10.8	47.0	27	17	AAQ15477	Primer for B7 open
c 433	11	47.8	50	22	AAQ31600	Human SNP oligonuc	506	10.8	47.0	27	19	AAQ31778	Nucleotide sequenc
c 434	11	47.8	50	22	AAQ31601	Human SNP oligonuc	507	10.8	47.0	27	21	AAQ59847	HSV thymidine kina
c 435	11	47.8	50	22	AAQ33541	Human SNP oligonuc	c 508	10.8	47.0	28	19	AAQ67174	Oligonucleotide SE
c 436	10.8	47.0	16	20	AAQ57818	PCR primer for G.	c 509	10.8	47.0	28	19	AAQ61886	Plasmid pET-7 prom
c 437	10.8	47.0	17	20	AAQ57838	PCR primer for G.	510	10.8	47.0	29	15	AAQ69969	Degenerate primer
c 438	10.8	47.0	19	21	AAQ82830	cdk4 ribozyme bind	511	10.8	47.0	29	17	AAQ39992	Primer back p1 for
c 439	10.8	47.0	19	22	AAQ57992	Celli-cycle depende	c 512	10.8	47.0	29	20	AAA21830	Integrin subunit b
c 440	10.8	47.0	20	20	AAQ202322	PCR primer used to	c 513	10.8	47.0	29	21	AAA04102	Polymorphic fragme
c 441	10.8	47.0	20	20	AAQ79780	PCR primer H14909	c 514	10.8	47.0	29	22	AAQ20324	S. pneumoniae murM
c 442	10.8	47.0	20	22	AAQ19437	Human delta-6-dea	515	10.8	47.0	29	24	AAQ17237	Upstream PCR prime
c 443	10.8	47.0	20	22	AAQ76129	Human tau gene 5'	c 516	10.8	47.0	30	15	AAQ66191	Primer for seven t
c 444	10.8	47.0	20	22	AAQ70526	Human DRD2 fragmen	517	10.8	47.0	30	15	AAQ66192	Primer for seven t
c 445	10.8	47.0	20	22	AAQ27518	G.ardea target seq	518	10.8	47.0	30	16	AAQ92607	Thermus thermophil
c 446	10.8	47.0	20	24	ABI93003	Capture oligonucle	c 519	10.8	47.0	30	18	AAQ58425	Apolipoprotein B g
c 447	10.8	47.0	20	24	ABI94897	Capture oligonucle	c 520	10.8	47.0	30	19	AAV18386	Human R20 seven tr

521	10.8	47.0	30	19	AAV18387	Human R20 seven tr	594	10.8	47.0	21	AAZ67019	Human map-related
522	10.8	47.0	30	20	AAV84889	PCR primer for hum	595	10.8	47.0	21	AAZ69480	Human map-related
c 523	10.8	47.0	30	20	AAV82536	Probe ApoB-1 used	c 596	10.8	47.0	48	AAV67171	pET-7 T7 promoter
c 524	10.8	47.0	30	21	AAV91738	Human 7TM receptor	c 597	10.8	47.0	48	AAV61893	Plasmid pET-7 prom
c 525	10.8	47.0	30	21	AAV91739	Human 7TM receptor	c 598	10.8	47.0	49	AAV91016	Human chromosome 4
c 526	10.8	47.0	30	21	AAZ47329	PCR primer Sextole	c 599	10.8	47.0	49	AAZ94248	Plasmid pRAE-6 elo
527	10.8	47.0	30	22	AAH27627	Human histone deac	600	10.8	47.0	50	AAQ69629	Human metallothion
528	10.8	47.0	30	22	AAF32187	Human oestrogen re	601	10.8	47.0	50	AAQ64091	Human metallothion
529	10.8	47.0	30	22	AAF26871	3'-mer oligonucleo	602	10.8	47.0	50	AAV66666	Anti-human Fas hum
c 530	10.8	47.0	31	16	AAQ91866	Murine trkB tyrosi	603	10.8	47.0	50	AAV19377	PCR primer R370-98
c 531	10.8	47.0	31	20	AAV60079	3' untranslated re	604	10.8	47.0	50	AAV19378	PCR primer R371-98
532	10.8	47.0	31	21	AAV73204	Human genomic DNA	605	10.8	47.0	50	AAV17379	Test sequence from
533	10.8	47.0	31	22	AAI30877	Human single nucle	606	10.8	47.0	50	AAV78357	Humanised anti-Fas
c 534	10.8	47.0	31	23	ABI97848	Non-endogenous hum	c 607	10.8	47.0	50	AAZ28696	Human SNP oligonuc
c 535	10.8	47.0	31	23	ABI97849	Non-endogenous hum	608	10.8	47.0	50	AAZ29849	Human SNP oligonuc
c 536	10.8	47.0	32	21	AAV73111	Human MC1R gene re	c 609	10.8	47.0	50	AAZ30002	Human SNP oligonuc
c 537	10.8	47.0	32	21	AAZ88085	Human interleukin	610	10.8	47.0	50	AAZ34018	Human SNP oligonuc
c 538	10.8	47.0	32	21	AAZ58560	Human interleukin	611	10.8	47.0	50	AAZ34195	Human SNP oligonuc
c 539	10.8	47.0	32	21	AAZ29035	Txin 2 gene-specif	612	10.8	47.0	50	AAZ34547	Human SNP oligonuc
c 540	10.8	47.0	32	23	ABI97850	Non-endogenous hum	c 613	10.8	47.0	50	AAI76887	Human silent SNP c
541	10.8	47.0	32	23	ABI97851	Non-endogenous hum	614	10.8	47.0	50	AAH89831	Human coding sequ
542	10.8	47.0	33	15	AAV70858	Foldback triplex-f	615	10.6	46.1	18	AAQ37154	Probe to detect GM
543	10.8	47.0	33	20	AAV60068	3' untranslated re	c 616	10.6	46.1	18	AAQ56863	PCR primer 17 for
544	10.8	47.0	34	17	AAV04400	PHENH6 primer #1.	c 617	10.6	46.1	18	AAI12894	Human Rb1 (retinob
c 545	10.8	47.0	34	19	AAV00259	Cloned psi 10 prom	618	10.6	46.1	18	AAV08005	Probe GM-CSF for I
c 546	10.8	47.0	34	20	AAV01916	Bacteriophage T7 R	c 619	10.6	46.1	19	AAH89909	AE-labelled RNA pr
547	10.8	47.0	34	22	AAI66425	Kringle protein 13	c 620	10.6	46.1	19	AAZ11027	Probe #7 to detect
c 548	10.8	47.0	35	20	AAV57526	TGMV coat protein	c 621	10.6	46.1	19	AAZ11290	Mycobacterium aviu
c 549	10.8	47.0	36	20	AAV79331	P. furiosus endonuc	c 622	10.6	46.1	20	AAQ37772	HCY universal olig
550	10.8	47.0	36	22	AAV24447	C. thermoaminoogen	c 623	10.6	46.1	20	AAQ080805	HCY genotype deter
551	10.8	47.0	36	22	AAV24449	C. thermoaminoogen	c 624	10.6	46.1	20	AAQ76004	IRS-1 PCR primer.
552	10.8	47.0	36	22	AAV74289	Arabidopsis calcicu	625	10.6	46.1	20	AAZ03245	PCR primer used to
553	10.8	47.0	37	22	AAV14067	Vector PADAP/ST-AR	c 626	10.6	46.1	20	AAV45609	Primer for Mycobac
c 554	10.8	47.0	37	22	AAV14068	Vector PADAP/ST-AR	c 627	10.6	46.1	20	AAV45608	Primer for Mycobac
c 555	10.8	47.0	38	20	AAV19407	Rat polyosome mRNA	c 628	10.6	46.1	20	AAZ44505	M. tuberculosis 16
556	10.8	47.0	39	15	AAZ70857	Foldback triplex-f	629	10.6	46.1	20	AAV72958	Human daxx inhibit
c 557	10.8	47.0	39	20	AAZ23561	RNAse T1 PCR prime	c 630	10.6	46.1	20	AAV91054	Human daxx inhibit
558	10.8	47.0	39	20	AAV35486	Upstream primer CT	c 631	10.6	46.1	20	AAV31802	Human RANK antise
c 559	10.8	47.0	39	20	AAV26505	WO 9909191 SeqID #	c 632	10.6	46.1	20	ABF95386	Capture oligonucle
560	10.8	47.0	39	21	AAZ35580	Amplification prim	c 633	10.6	46.1	20	ABF95781	Capture oligonucle
561	10.8	47.0	40	18	AAV17339	Primer 96 used in	c 634	10.6	46.1	20	ABA02830	Mycobacterium tub
c 562	10.8	47.0	40	18	AAV87163	IFN-gamma 2'F/NH2	635	10.6	46.1	21	AAQ40069	E. coli 16S rRNA o
c 563	10.8	47.0	40	22	AAV74442	PCR primer used to	c 636	10.6	46.1	21	AAV57651	Exon 9 of an ENAC
564	10.8	47.0	41	19	AAV50844	Maize polymorphic	637	10.6	46.1	21	AAV51075	Bacterial 16S RNA
565	10.8	47.0	41	19	AAV47702	Maize polymorphic	c 638	10.6	46.1	22	AAQ52620	Primer Y673S huHG
566	10.8	47.0	41	20	AAV19298	Human granulocyte	639	10.6	46.1	22	AAV72015	Primer detects mar
c 567	10.8	47.0	41	22	AAV48082	Ras GTPase-activat	640	10.6	46.1	22	AAV71943	Primer detects mar
568	10.8	47.0	42	19	AAV05421	Primer used in pro	c 641	10.6	46.1	22	AAV48447	Transforming grow
569	10.8	47.0	42	20	AAZ25254	Caspase-3 PCR prim	c 642	10.6	46.1	22	AAV15641	Primer used to gen
570	10.8	47.0	42	21	AAV22881	VEGF gene PCR prim	643	10.6	46.1	22	AAV66585	Gene typing PCR pr
571	10.8	47.0	42	21	AAV5854	VEGF PCR primer SE	c 644	10.6	46.1	22	AAV11298	Human ANK gene PCR
c 572	10.8	47.0	43	21	AAZ44610	Transcription vect	645	10.6	46.1	22	AAV89963	Human ANK gene PCR
c 573	10.8	47.0	43	22	AAV61144	B. napus HPPD PCR	c 646	10.6	46.1	23	AAV66556	PCR primer used to
c 574	10.8	47.0	44	19	AAV11490	A. niger transposa	c 647	10.6	46.1	23	AAV38492	Oligonucleotide 10
575	10.8	47.0	44	20	AAZ30897	Oligonucleotide WF	c 648	10.6	46.1	23	AAV11292	Human beta-globin
c 576	10.8	47.0	44	22	AAZ82186	Human retrovirus D	649	10.6	46.1	24	AAI36712	Human ANK gene PCR
577	10.8	47.0	45	19	AAV38167	Oligonucleotide-81	650	10.6	46.1	24	AAV00171	Downstream primer
c 578	10.8	47.0	45	19	AAV38168	Oligonucleotide-82	c 651	10.6	46.1	24	AAV00171	Human CD8 PCR anti
c 579	10.8	47.0	45	19	AAV11489	A. niger transposa	652	10.6	46.1	24	ABF87342	Capture oligonucle
c 580	10.8	47.0	45	20	AAV82032	Mouse heavy chain	c 653	10.6	46.1	24	ABF87343	Capture oligonucle
c 581	10.8	47.0	45	20	AAV82013	Mouse heavy chain	654	10.6	46.1	24	ABF88132	Capture oligonucle
c 582	10.8	47.0	45	20	AAV05563	Mouse heavy chain	655	10.6	46.1	24	ABF88133	Capture oligonucle
c 583	10.8	47.0	45	20	AAV03242	PCR primer used to	656	10.6	46.1	24	ABF89176	Capture oligonucle
c 584	10.8	47.0	45	22	AAV01740	Exochitinase gene	c 657	10.6	46.1	25	AAV66555	Oligonucleotide 10
c 585	10.8	47.0	45	22	AAV87059	Probe used to isol	c 658	10.6	46.1	25	AAV60406	Primer CRE3fused t
586	10.8	47.0	46	15	AAV6948	Human genome fragm	659	10.6	46.1	25	AAV65589	Glomerular fibron
587	10.8	47.0	46	16	AAV084392	Mycobacterium smeg	c 660	10.6	46.1	25	AAV38491	Human beta-globin
588	10.8	47.0	46	19	AAV68584	Nucleotide sequenc	661	10.6	46.1	26	AAA91664	HCV(+)-RNA oligonuc
589	10.8	47.0	46	19	AAV01774	C. trachomatis cry	662	10.6	46.1	27	AAQ24380	PCR primer C. Syn
590	10.8	47.0	46	20	AAV78455	Primer 2. Synthet	663	10.6	46.1	27	AAV19054	Tetracycline knock
591	10.8	47.0	46	20	AAV30266	Chlamydia cryptic	664	10.6	46.1	27	AAV68656	Nucleotide sequenc
592	10.8	47.0	46	20	AAV30007	Amplification prim	665	10.6	46.1	27	AAH43364	MIP-2 (antisense)
593	10.8	47.0	46	20	AAV82662	Amplification prim	666	10.6	46.1	27	AAV25783	S. chrysomallus AC

c 667	10.6	46.1	28	16	AAQ94138	HML(R153A,R154A),	740	10.6	46.1	42	21	AAQ65243	Allele-specific st
c 668	10.6	46.1	29	16	AAQ94139	HML(R153A,R154A),	741	10.6	46.1	42	21	AAA65065	Exemplary HaNS3 e
c 669	10.6	46.1	28	20	AAA16822	Aryl hydrocarbon n	742	10.6	46.1	42	22	AAQ63634	SDA primer haensda
c 670	10.6	46.1	29	20	AAA16995	Aryl hydrocarbon n	743	10.6	46.1	42	22	AAQ64894	Novel strand displ
c 671	10.6	46.1	29	20	AAA19728	Integrin alpha 6 s	c 744	10.6	46.1	43	19	AAV33648	Plasmids pVLSNOSIB
c 672	10.6	46.1	29	21	AAA24229	Oestrogen receptor	745	10.6	46.1	43	19	AAV33646	Mouse VL30 promote
c 673	10.6	46.1	29	21	AAA04241	Polymorphic fragme	c 746	10.6	46.1	43	21	AAZ94644	Mutagenic primer H
c 674	10.6	46.1	29	21	AAA04563	Polymorphic fragme	747	10.6	46.1	43	21	AAZ94645	Mutagenic primer H
c 675	10.6	46.1	30	20	AAZ55487	Oligonucleotide RB	c 748	10.6	46.1	43	22	AAQ16433	Human alpha-3 IV c
c 676	10.6	46.1	30	22	AAZ54460	Primer used to gen	749	10.6	46.1	43	12	AAQ10551	Bone calcification
c 677	10.6	46.1	30	22	AAZ54468	Primer used to gen	c 750	10.6	46.1	45	20	AAZ32422	scFv 12B5 heavy ch
c 678	10.6	46.1	31	19	AAV19852	Primer for human 1	c 751	10.6	46.1	45	20	AAZ32425	PCR primer used to
c 679	10.6	46.1	31	20	AAQ02652	EP-892047 Seq ID 2	752	10.6	46.1	45	21	AAZ94996	E. tenella small r
c 680	10.6	46.1	31	21	AAZ94375	Caenorhabditis ele	c 753	10.6	46.1	45	21	AAQ01235	Biotin-binding pep
c 681	10.6	46.1	31	22	AAI31153	Human single nucle	754	10.6	46.1	46	15	AAQ69394	Human growth hormo
c 682	10.6	46.1	32	15	AAQ63989	Mouse low-density	c 755	10.6	46.1	46	18	AAQ63856	Human growth hormo
c 683	10.6	46.1	32	16	AAQ03449	Human LAG-3 extrac	c 756	10.6	46.1	46	20	AAQ17144	Test sequence from
c 684	10.6	46.1	33	13	AAQ31161	Probe 130 for geno	c 757	10.6	46.1	47	14	AAQ34665	H-ras sense primer
c 685	10.6	46.1	33	14	AAQ46467	Hepatitis C virus	c 758	10.6	46.1	47	14	AAQ46361	PCR sense primer t
c 686	10.6	46.1	33	19	AAV07841	HCV.33.12 amplifie	c 759	10.6	46.1	47	18	AAQ36445	PCR primer for H-r
c 687	10.6	46.1	33	20	AAV83069	Amplifier probe HC	c 760	10.6	46.1	47	19	AAV07874	H-ras gene sense p
c 688	10.6	46.1	33	22	AAH73956	Human molybdenum p	c 761	10.6	46.1	47	20	AAQ10299	PCR primer used to
c 689	10.6	46.1	33	22	AAQ89168	p-HYDE sequence fr	762	10.6	46.1	47	20	AAZ52585	Human genome blall
c 690	10.6	46.1	33	24	ABA05154	Human cannabinoid	c 763	10.6	46.1	47	20	AAZ15089	PCR primer used to
c 691	10.6	46.1	34	19	AAV37234	PCR primer for mou	c 764	10.6	46.1	47	20	AAZ05489	Human H-ras gene f
c 692	10.6	46.1	34	20	AAZ52452	Forward PCR primer	c 765	10.6	46.1	47	21	AAZ68661	Human map-related
c 693	10.6	46.1	34	21	AAA46915	PCR primer used to	c 766	10.6	46.1	47	21	AAZ68991	Human map-related
c 694	10.6	46.1	34	22	AAZ72610	Human PRO polypept	c 767	10.6	46.1	47	21	AAZ68913	Exemplary oligonuc
c 695	10.6	46.1	35	18	AAZ50850	Blocking oligonuc	c 768	10.6	46.1	47	21	AAZ48150	Human H-ras PCR pr
c 696	10.6	46.1	35	22	AAZ75846	Porcine circovirus	769	10.6	46.1	48	12	AAQ12252	HIV-1 LTR mutation
c 697	10.6	46.1	35	22	AAZ87666	PCV-1 virus ORF2 g	c 770	10.6	46.1	48	20	AAZ99203	M. dovis 16S rRNA
c 698	10.6	46.1	35	24	ABA02829	Mycobacterium tube	c 771	10.6	46.1	48	20	AAZ99204	M. avium 16S rRNA
c 699	10.6	46.1	36	13	AAQ21153	Sequence of DNA do	c 772	10.6	46.1	48	20	AAZ99202	M. tuberculosis 16
c 700	10.6	46.1	36	18	AAZ91801	Target binding seq	c 773	10.6	46.1	48	20	AAZ85972	PRO cDNA amplifica
c 701	10.6	46.1	36	19	AAZ20589	Bovine ADAM 10 PCR	774	10.6	46.1	49	16	AAQ98124	Label extender pro
c 702	10.6	46.1	36	20	AAZ87666	Hepatocyte growth	775	10.6	46.1	50	22	AAQ217862	Human SNP oligonuc
c 703	10.6	46.1	36	20	AAZ73945	Human TNF-alpha co	776	10.6	46.1	50	22	AAQ217863	Human SNP oligonuc
c 704	10.6	46.1	36	21	AAZ89286	Human tissue bindi	777	10.6	46.1	50	22	AAQ28001	Human SNP oligonuc
c 705	10.6	46.1	36	22	AAZ46635	DNA encoding flag	c 778	10.6	46.1	50	22	AAQ30328	Human SNP oligonuc
c 706	10.6	46.1	37	18	AAZ79536	Jun leucine zipper	779	10.6	46.1	50	22	AAQ32133	Human SNP oligonuc
c 707	10.6	46.1	37	22	AAZ75898	Human papillomavir	780	10.6	46.1	50	22	AAQ32134	Human SNP oligonuc
c 708	10.6	46.1	38	14	AAQ36869	PCR primer for D.	781	10.6	46.1	50	22	AAQ32421	Human SNP oligonuc
c 709	10.6	46.1	38	18	AAZ91804	Target binding seq	782	10.6	46.1	50	22	AAQ33859	Human SNP oligonuc
c 710	10.6	46.1	39	19	AAV16821	Mycobacterium kans	783	10.6	46.1	50	22	AAQ34612	Human SNP oligonuc
c 711	10.6	46.1	39	22	AAH41065	PCR primer specifi	c 784	10.6	46.1	50	22	AAQ20061	M. avium 16S rRNA
c 712	10.6	46.1	40	17	AAZ37089	ELAF matrix metall	785	10.6	46.1	50	22	AAZ86977	Probe used to iden
c 713	10.6	46.1	40	18	AAZ90816	Primer P2 for C. p	c 786	10.4	45.2	13	20	AAV63773	Human JAGGED1 exon
c 714	10.6	46.1	40	19	AAV16820	Mycobacterium kans	c 787	10.4	45.2	15	21	AAZ62568	Substrate for HH r
c 715	10.6	46.1	40	21	AAZ87834	Amplification prim	788	10.4	45.2	18	16	AAQ76214	HSV L/ST primer.
c 716	10.6	46.1	40	21	AAZ87839	HRP conjugated P2	789	10.4	45.2	19	20	AAZ72572	Thyroid peroxidase
c 717	10.6	46.1	40	21	AAZ46372	PCR primer used to	790	10.4	45.2	19	21	AAZ89345	Human UCP3 protein
c 718	10.6	46.1	40	21	AAZ46374	Oligonucleotide pr	791	10.4	45.2	19	24	ABA81947	Rat G-protein sero
c 719	10.6	46.1	40	21	AAZ95917	Polynucleotide seq	792	10.4	45.2	20	15	AAQ62996	Angiotensinogen mo
c 720	10.6	46.1	40	22	AAZ14554	Arabidopsis thalia	793	10.4	45.2	20	19	AAZ85725	LRP5 exon primer E
c 721	10.6	46.1	40	22	AAZ14567	Arabidopsis thalia	794	10.4	45.2	20	19	AAZ23973	Primer for detecti
c 722	10.6	46.1	40	22	AAZ07859	Binding site selec	795	10.4	45.2	20	20	AAZ05556	PCR primer used to
c 723	10.6	46.1	40	22	AAZ07872	DNA ligand #19 for	796	10.4	45.2	20	21	AAZ11896	Human MDMX antisen
c 724	10.6	46.1	40	22	AAQ10613	Arabidopsis thalia	797	10.4	45.2	20	21	AAZ60310	Forward primer spe
c 725	10.6	46.1	40	22	AAZ08927	Arabidopsis thalia	c 798	10.4	45.2	20	21	AAZ46580	Human angiotensino
c 726	10.6	46.1	40	22	AAZ08940	Arabidopsis thalia	799	10.4	45.2	20	21	AAZ38440	Human adenosine A2
c 727	10.6	46.1	40	22	AAZ03339	A group IA abscisi	c 800	10.4	45.2	20	22	AAZ76267	PCR primer used to
c 728	10.6	46.1	40	22	AAZ03332	ABRE binding seque	801	10.4	45.2	20	22	AAH42437	Human angiotensino
c 729	10.6	46.1	40	22	AAZ00392	ABRE binding seque	802	10.4	45.2	20	22	AAQ67110	Capture oligonucle
c 730	10.6	46.1	40	22	AAZ00405	PCR primer OPR136	803	10.4	45.2	20	24	AAZ97356	Oligo #27 for ampl
c 731	10.6	46.1	41	17	AAZ34716	Human diacylglycer	c 804	10.4	45.2	21	20	AAZ17756	Forward primer #44
c 732	10.6	46.1	41	22	AAH46537	Human peroxidase a	c 805	10.4	45.2	21	21	AAZ80173	Human prostate spe
c 733	10.6	46.1	41	22	AAZ64912	Guinea pig histami	806	10.4	45.2	21	21	AAZ76046	Human prostate spe
c 734	10.6	46.1	41	24	AAZ71001	Human G2 activati	807	10.4	45.2	21	21	AAZ76055	Drosophila Na+ dri
c 735	10.6	46.1	41	24	ABA92344	Ribosomal S3 prote	808	10.4	45.2	21	21	AAZ93746	Anchored PCR prim
c 736	10.6	46.1	41	24	ABA04976	Novel strand displ	809	10.4	45.2	21	22	AAZ07187	PCR primer for cDN
c 737	10.6	46.1	42	21	AAZ63153	Novel strand displ	810	10.4	45.2	21	22	AAH42163	Cholinergic recept
c 738	10.6	46.1	42	21	AAZ64832	Novel strand displ	811	10.4	45.2	21	22	AAH62434	Human gene single
c 739	10.6	46.1	42	21	AAZ65176	Novel strand displ	c 812	10.4	45.2	21	22	AAZ97279	

813	10.4	45.2	21	22	AAF97630	Human gene single	c 886	10.4	45.2	30	20	AAx85758	PCR primer used to
814	10.4	45.2	21	22	AAF59583	Mouse urotensin II	c 887	10.4	45.2	30	20	AAx85761	PCR primer used to
c 815	10.4	45.2	21	23	ABA10180	Tail primer #173 f	888	10.4	45.2	30	20	AAx58601	Human cancer anti
c 816	10.4	45.2	22	16	AAAT05920	COX II sense probe	889	10.4	45.2	30	21	AAx30700	Human HG38 (V765K)
817	10.4	45.2	22	18	AAAT76319	Human muscarinic a	890	10.4	45.2	30	21	AAZ94325	Rat neurotensin Nt
818	10.4	45.2	22	20	AAZ25147	Human short inters	c 891	10.4	45.2	30	21	AAZ61196	Probe C12C151 use
819	10.4	45.2	22	20	AAZ25157	Human short inters	c 892	10.4	45.2	30	22	AAc85831	Primer #3 used in
820	10.4	45.2	22	20	AAZ25158	Human short inters	c 893	10.4	45.2	30	22	AAf77267	Primer X specific
821	10.4	45.2	22	21	AAx54117	Muscarinic acetylch	c 894	10.4	45.2	30	22	AAf31885	Hamster Ku86 PCR p
c 822	10.4	45.2	22	21	AAx80174	Forward primer #45	c 895	10.4	45.2	31	14	AAQ51483	Dengue virus sequ
c 823	10.4	45.2	22	21	AAf19683	Human muscarinic a	c 896	10.4	45.2	31	20	AAZ23224	HCV NS5B DNA speci
c 824	10.4	45.2	22	21	AAA75912	PCR primer for CDN	c 897	10.4	45.2	31	21	AAA78849	Human genomic DNA
825	10.4	45.2	22	21	AAf76047	Human prostate spe	898	10.4	45.2	31	21	AAA58369	PCR primer pcDNA(S
826	10.4	45.2	22	21	AAA76060	Human prostate spe	899	10.4	45.2	31	22	AAI30457	Human single nucle
827	10.4	45.2	22	21	AAA33561	Low adenosine anti	900	10.4	45.2	31	22	AAI30458	Human single nucle
c 828	10.4	45.2	22	21	AAZ50750	3'HUMAN OCR10rc pr	901	10.4	45.2	31	22	AAI30552	Human single nucle
c 829	10.4	45.2	22	22	AAH74132	Oligonucleotide #5	902	10.4	45.2	32	15	AAQ67142	Primer for amplif
c 830	10.4	45.2	22	22	AAH50117	Bacterial 23S/5S R	c 903	10.4	45.2	32	15	AAQ71642	Apo-B RNA editing
c 831	10.4	45.2	22	23	AAAD21619	3' PCR-RFLP modifi	c 904	10.4	45.2	32	15	AAQ87875	Component B gene p
c 832	10.4	45.2	23	17	AAAT35856	Prostate-specific	905	10.4	45.2	32	16	AAAT00830	HIV-1 HXB2 envelop
c 833	10.4	45.2	23	18	AAAT59518	Porcine CD34 forwa	c 906	10.4	45.2	32	16	AAQ84709	Non-specific unive
c 834	10.4	45.2	23	21	AAc80175	Forward primer #46	907	10.4	45.2	32	17	AAAT32896	Human immunodefici
c 835	10.4	45.2	24	18	AAAT78855	340 bp 5' lecithin	c 908	10.4	45.2	32	17	AAAT42572	Primer #3 for acut
c 836	10.4	45.2	24	19	AAV38028	SCEPO section 3 co	909	10.4	45.2	32	17	AAAT35019	TIMP-1/fibronectin
837	10.4	45.2	24	19	AAV38029	SCEPO section 3 co	c 910	10.4	45.2	32	18	AAAT64570	Primer for thymus
c 838	10.4	45.2	24	19	AAV26275	T. vaginalis homoc	911	10.4	45.2	32	18	AAAT84458	Heat shock protein
c 839	10.4	45.2	24	20	AAx35044	Oligonucleotide us	c 912	10.4	45.2	32	19	AAV41631	Nucleotide sequenc
c 840	10.4	45.2	24	21	AAc80176	Forward primer #47	c 913	10.4	45.2	32	20	AAx87365	Universal adaptor
841	10.4	45.2	24	21	AAZ93970	Primer used to gen	c 914	10.4	45.2	32	20	AAx22978	Canine En-2 primer
842	10.4	45.2	24	21	AAZ89689	Human ADAM DNA PCR	c 915	10.4	45.2	32	20	AAx06681	Antisense universa
c 843	10.4	45.2	24	21	AAZ39745	Human glycerinalde	c 916	10.4	45.2	32	21	AAAG6949	RACE PCR primer us
c 844	10.4	45.2	24	22	AAf30649	Human HDGFX hybrid	c 917	10.4	45.2	32	21	AAc64094	Universal adapter
c 845	10.4	45.2	24	22	AAf30652	Human HDGFX hybrid	c 918	10.4	45.2	32	21	AAx88573	Universal amplific
c 846	10.4	45.2	24	22	AAf25450	Oligonucleotide us	c 919	10.4	45.2	32	21	AAZ51330	Universal amplifi
c 847	10.4	45.2	24	24	AB184780	Capture oligonucle	c 920	10.4	45.2	32	21	AAZ51330	Soluble herpesviro
c 848	10.4	45.2	24	24	AB184781	Capture oligonucle	921	10.4	45.2	32	21	AAH294199	Human IL-6 promote
c 849	10.4	45.2	24	24	AB186024	Capture oligonucle	c 922	10.4	45.2	32	22	AAH22975	Primer used to amp
c 850	10.4	45.2	24	24	AB186025	Capture oligonucle	c 923	10.4	45.2	32	22	AAH25201	Human homologous p
851	10.4	45.2	24	24	AB191282	Capture oligonucle	c 924	10.4	45.2	32	22	AAH04959	Rainbow trout prep
c 852	10.4	45.2	24	24	AB191283	Capture oligonucle	925	10.4	45.2	32	22	AAH12938	Probe 84 specific
c 853	10.4	45.2	25	14	AAQ37580	HCV conserved regi	926	10.4	45.2	33	13	AAQ31115	Probe 126 for geno
c 854	10.4	45.2	25	18	AAAT64894	Hepatitis C virus	927	10.4	45.2	33	14	AAQ46421	Hepatitis C virus
c 855	10.4	45.2	25	19	AAV53718	Nucleotide sequenc	928	10.4	45.2	33	14	AAQ46463	Hepatitis C virus
c 856	10.4	45.2	25	21	AAc80177	Forward primer #48	929	10.4	45.2	33	19	AAV07837	HCV 33.8 amplifier
857	10.4	45.2	26	14	AAQ37585	HCV conserved regi	930	10.4	45.2	33	20	AAV83065	Amplifier probe HC
c 858	10.4	45.2	26	14	AAQ40270	Sequence of PCR pr	931	10.4	45.2	33	21	AAZ35996	CAT gene long rang
c 859	10.4	45.2	26	18	AAAT64899	Hepatitis C virus	c 932	10.4	45.2	33	21	AAZ35996	Human OATP-B PCR p
c 860	10.4	45.2	26	21	AAx89839	Primer od53. Synt	c 933	10.4	45.2	34	15	AAQ55228	Full length CD40 b
c 861	10.4	45.2	26	22	AAH12757	PCR primer oligonu	c 934	10.4	45.2	34	16	AAQ96202	Primer #2. Synthe
862	10.4	45.2	26	22	AAI65053	PCR primer #4. Un	935	10.4	45.2	34	16	AAQ88949	VEGF RNA nucleic a
c 863	10.4	45.2	27	9	AAH81250	Probe 0-34BHI to i	936	10.4	45.2	34	17	AAAT36515	Primer to amplify
c 864	10.4	45.2	27	9	AAH81250	Probe 0-34BHI for	c 937	10.4	45.2	34	18	AAAT79187	Human full length
c 865	10.4	45.2	27	14	AAQ36549	Encodes Arg rich i	938	10.4	45.2	34	20	AAx36577	PCR primer for hum
866	10.4	45.2	27	20	AAx58602	Human cancer anti	c 939	10.4	45.2	34	22	AAH13973	Shope Fibroma Viru
c 867	10.4	45.2	27	22	AAH42310	Primer for DNA enc	940	10.4	45.2	34	22	AAAD07438	Kaposi's sarcoma v
868	10.4	45.2	27	22	AAH19828	Synthetic DNA for	941	10.4	45.2	34	22	AAH00266	LPA receptor-relat
c 869	10.4	45.2	27	22	AAH19829	Synthetic DNA for	c 942	10.4	45.2	36	19	AAV45087	Human IL-12 primer
c 870	10.4	45.2	27	22	AAf30468	RT-PCR primer BA-F	c 943	10.4	45.2	36	21	AAV35922	Permutate linker e
c 871	10.4	45.2	27	22	AAf30469	RT-PCR primer BA-R	944	10.4	45.2	37	16	AAQ88954	VEGF RNA nucleic a
872	10.4	45.2	27	22	AAf24392	M tuberculosis Rv2	c 945	10.4	45.2	37	19	AAV26166	PRRS ORF2 gene PCR
873	10.4	45.2	28	22	AAAS59949	Canine IgG heavy c	946	10.4	45.2	37	22	AAH91190	Human inflammatory
874	10.4	45.2	28	22	AAH28148	PCR primer used to	c 947	10.4	45.2	37	22	AAf30198	Clone 11618130.0.2
875	10.4	45.2	29	20	AAx84022	PCR primer for HCV	c 948	10.4	45.2	37	22	AAf26091	Feline IL-12p35 PC
c 876	10.4	45.2	29	20	AAx84023	PCR primer for HCV	949	10.4	45.2	38	18	AAAT66670	Mycobacterium kans
c 877	10.4	45.2	29	21	AAf00251	Hammerhead ribozym	950	10.4	45.2	38	19	AAV85726	LRP5 exon primer E
c 878	10.4	45.2	29	21	AAA58398	Human VNTK5 PCR pr	951	10.4	45.2	38	20	AAZ00736	S. agalactiae GBS3
c 879	10.4	45.2	29	21	AAA04121	Polymorphic fragme	952	10.4	45.2	38	20	AAx24243	Oligonucleotide pr
880	10.4	45.2	29	21	AAZ36824	Probe TUB-1 used t	953	10.4	45.2	38	20	AAx24259	Oligonucleotide pr
881	10.4	45.2	29	22	AAH43955	Plasmid PBS-RSV mu	c 954	10.4	45.2	38	21	AAx49338	Primer used to amp
882	10.4	45.2	29	22	AAf25791	S. chrysomallus AC	c 955	10.4	45.2	38	22	AAH15528	Beta actin gene pr
c 883	10.4	45.2	29	22	AAI65151	Canine IL12p35 gen	956	10.4	45.2	38	22	AAH96845	Human Chk1 ribozym
884	10.4	45.2	29	23	AB197681	Endogenous human G	957	10.4	45.2	38	22	AAH96944	Human Chk1 ribozym
885	10.4	45.2	30	19	AAV66536	Reverse PCR primer	958	10.4	45.2	38	23	ABK05624	Human NOGO Zinzyne

CC treatment of tumors, autoimmune diseases, scar formation, inflammation,
 CC allergy, rheumatic diseases and defence against transplantation.
 CC AAZ43869-Z43871 represent primers described in the method of the
 CC invention.
 XX
 SQ Sequence 23 BP; 4 A; 7 C; 8 G; 4 T; 0 other;

Query Match 100.0%; Score 23; DB 21; Length 23;
 Best Local Similarity 100.0%; Pred. No. 0.096;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 accaggcgtctcgtggccacat 23
 |||||
 Db 23 ACCAGGCGTCTCGTGGCCACAT 1

RESULT 3
 AAQ58903
 ID AAQ58903 standard; DNA; 48 BP.

XX AC AAQ58903;

XX DT 26-OCT-1994 (first entry)

XX Human beta-glucuronidase cloning oligonucleotide Hum.B-Gluc back.

XX Carcinoembryonic antigen; single chain variable region; sfv fragment;
 KW fusion gene; cancer treatment; targeted drug delivery; tumour;
 KW beta-glucuronidase; prodrug activating enzyme; ss.

XX OS Synthetic.

XX PN EP590530-A.

XX PD 06-APR-1994.

XX PF 24-SEP-1993; 93EP-0115418.

XX PR 02-OCT-1992; 92DE-4233152.

XX PA (BEHW) BEHRINGERWERKE AG.

XX PI Bosslet K, Czech J, Gehrman M, Seemann G;

XX WPI; 1994-111012/14.

PT New fusion protein contg. enzyme for prodrug activation - coupled
 PT to antigen binding component, esp. sfv antibody fragment, partic.
 PT for treatment of tumours

XX PS Example 10; Page 20; 35pp; German.

XX Oligonucleotides Hum.B-Gluc back (AAQ58903) and Hum.B-Gluc for
 CC (AAQ58904) were used for cloning the human beta-glucuronidase gene into
 CC a pUC19 vector all ready containing an anti-CEA single chain antibody
 CC construct sfv 431/26. The resultant fusion protein is useful for
 CC targeting beta-glucuronidase to cancer cells expressing CEA, where
 CC the enzyme is able to convert a prodrug into its active form.

XX SQ Sequence 48 BP; 14 A; 11 C; 16 G; 7 T; 0 other;

Query Match 63.5%; Score 14.6; DB 15; Length 48;
 Best Local Similarity 81.0%; Pred. No. 1e+03;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 ccaggcgtctcgtggccaca 22
 |||||

Db 12 caaagcgtcgtggccaca 32

RESULT 4

AAQ04776/c
 ID AAX04776 standard; DNA; 30 BP.

XX AC AAX04776;

XX DT 09-APR-1999 (first entry)

XX PCR primer of the invention.

XX Acremonium sp. S4G13; glucose transfer; sugar transferase
 KW sugar receptor; starch; PCR primer; ss.

XX OS Synthetic.

XX PN JP11009276-A.

XX PD 19-JAN-1999.

XX PF 19-JUN-1997; 97JP-0163110.

XX PR 19-JUN-1997; 97JP-0163110.

XX PA (KIRI) KIRIN BREWERY KK.

XX WPI; 1999-145893/13.

XX New sugar transferase gene and enzyme - useful for catalysing the
 PT transfer of an alpha-1 right arrow 3 bond to a sugar receptor for
 PT saccharide preparation

XX Example 6; Page 11; 20pp; Japanese.

XX The present PCR primer was used in the course of the invention. The
 CC specification describes a sugar transferase protein of Acremonium
 CC sp. S4G13. The protein preferably catalyses the glucose transfer of an
 CC alpha-1 right arrow 3 bond or the glucose transfer of an alpha-1 right
 CC arrow 3 and an alpha-1 right arrow 4 bond to a sugar receptor by
 CC reacting with a substrate selected from starch and its decomposition
 CC products.

XX SQ Sequence 30 BP; 5 A; 12 C; 8 G; 5 T; 0 other;

Query Match 61.7%; Score 14.2; DB 20; Length 30;
 Best Local Similarity 84.2%; Pred. No. 1.5e+03;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 accaggcgtctcgtggcc 19

|||||
 Db 25 ACCAGGCGTTCGTGGGCC 7

RESULT 5

AAQ28873/c
 ID AAL28873 standard; DNA; 50 BP.

XX AC AAL28873;

XX DT 24-JAN-2002 (first entry)

XX Human SNP oligonucleotide #2081.

XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
 KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
 KW cyclin; polymerase; angiopoietin; apoptosis related protein; adhering;
 KW complement related protein; cytochrome; kinase; colony stimulating factor;
 KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
 KW multifactorial disease; autoimmune disease; infection;
 KW nervous system disease; ss.

XX Homo sapiens.

XX OS

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PN  WO200147944-A2.
XX
PD  05-JUL-2001.
XX
PF  28-DEC-2000; 2000WO-US35498.
XX
PR  28-DEC-1999; 99US-0173419.
XX
PR  27-DEC-2000; 2000US-0173419.
XX
PA  (CURA-) CURAGEN CORP.
XX
PI  Shimkets RA, Leach M;
XX
PI  WPI; 2001-465210/50.
XX
XX  Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
PT  oncogenes and histones, useful for diagnosing and treating, e.g.
PT  cancer, autoimmune diseases and infections -
XX
PS  Claim 1; Page 1977; 4143pp; English.
XX
XX  The present invention relates to oligonucleotides encoding polymorphic
CC  variants of proteins related to amylases, amyloid proteins, angiotensin,
CC  apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
CC  histones, kinases, colony stimulating factors, complement related
CC  proteins, cytochromes, kinesins, cytokines, interferons, interleukins,
CC  G-protein coupled receptors and thioesterases. The present sequence is
CC  one such oligonucleotide. The oligonucleotides and the peptides encoded
CC  by them may be used in the prevention, diagnosis and treatment of
CC  diseases associated with inappropriate expression of the proteins listed
CC  above. Disorders that may be prevented, diagnosed and/or treated include
CC  multifactorial diseases with a genetic component, such as autoimmune
CC  diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
CC  systemic lupus erythematosus and Grave's disease), inflammation, cancer
CC  (e.g. cancers of the bladder, brain, breast, colon and kidney,
CC  leukaemia), diseases of the nervous system and an infection of pathogenic
CC  organisms.
XX
SQ  Sequence 50 BP; 9 A; 17 C; 19 G; 5 T; 0 other;

      Query Match      60.9%; Score 14; DB 22; Length 50;
      Best Local Similarity 77.3%; Pred. No. 2e+03;
      Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy  2 ccaggcgtctcgtggccacat 23
    |||| || | |||| || |||
Db  35 CCAGCGCGCGGTGGCCCTCAT 14

RESULT 6
AAL28874/c
ID  AAL28874 standard; DNA; 50 BP.
XX
AC  AAL28874;
XX
XX  24-JAN-2002 (first entry)
XX
DE  Human SNP oligonucleotide #2082.
XX
XX  Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW  neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
KW  amyloid protein; angiotensin; apoptosis related protein; cadherin;
KW  cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW  complement related protein; cytochrome; kinesin; cytokine; interferon;
KW  interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW  multifactorial disease; autoimmune disease; infection;
KW  nervous system disease; ss.
XX
OS  Homo sapiens.
XX
XX  WO200147944-A2.
XX
XX

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PD  05-JUL-2001.
XX
XX  28-DEC-2000; 2000WO-US35498.
XX
PR  28-DEC-1999; 99US-0173419.
XX
PR  27-DEC-2000; 2000US-0173419.
XX
PA  (CURA-) CURAGEN CORP.
XX
PI  Shimkets RA, Leach M;
XX
PI  WPI; 2001-465210/50.
XX
XX  Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
PT  oncogenes and histones, useful for diagnosing and treating, e.g.
PT  cancer, autoimmune diseases and infections -
XX
PS  Claim 1; Page 1977; 4143pp; English.
XX
XX  The present invention relates to oligonucleotides encoding polymorphic
CC  variants of proteins related to amylases, amyloid proteins, angiotensin,
CC  apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
CC  histones, kinases, colony stimulating factors, complement related
CC  proteins, cytochromes, kinesins, cytokines, interferons, interleukins,
CC  G-protein coupled receptors and thioesterases. The present sequence is
CC  one such oligonucleotide. The oligonucleotides and the peptides encoded
CC  by them may be used in the prevention, diagnosis and treatment of
CC  diseases associated with inappropriate expression of the proteins listed
CC  above. Disorders that may be prevented, diagnosed and/or treated include
CC  multifactorial diseases with a genetic component, such as autoimmune
CC  diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
CC  systemic lupus erythematosus and Grave's disease), inflammation, cancer
CC  (e.g. cancers of the bladder, brain, breast, colon and kidney,
CC  leukaemia), diseases of the nervous system and an infection of pathogenic
CC  organisms.
XX
SQ  Sequence 50 BP; 9 A; 16 C; 19 G; 6 T; 0 other;

      Query Match      60.9%; Score 14; DB 22; Length 50;
      Best Local Similarity 77.3%; Pred. No. 2e+03;
      Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy  2 ccaggcgtctcgtggccacat 23
    |||| || | |||| || |||
Db  34 CCAGCGCGCGGTGGCCCTCAT 13

RESULT 7
AAQ79883/c
ID  AAQ79883 standard; cDNA; 34 BP.
XX
AC  AAQ79883;
XX
XX  17-JUL-1995 (first entry)
XX
DE  Adrenodoxin-reductase primer 8.
XX
XX  P450sc: P450 side chain cleavage enzyme; fusion enzyme;
KW  electron-transfer protein; transgenic animal; cholesterol;
KW  atherosclerosis; adrenodoxin-reductase; AdRed; adrenodoxin; Adx;
KW  polymerase chain reaction; PCR; amplification; primer; ss.
XX
OS  Synthetic.
XX
XX  WO9429434-A.
XX
XX  22-DEC-1994.
XX
XX  09-JUN-1994; 94WO-US06698.
XX
XX  09-JUN-1993; 93US-0075193.
XX
XX

```

PA (REGC) UNIV CALIFORNIA.
 XX Black SM, Hari Krishna JA, Miller WL;
 XX WPI; 1995-036464/05.
 XX Fusion enzyme comprising P450sc and an electron-transfer protein
 PT - used in the production of transgenic livestock with reduced
 PT cholesterol meat
 XX
 PS Example 1; Page 37; 91pp; English.
 XX
 CC The primers given in AAQ79878-85 were used to engineer human cDNAs
 CC for P450sc, adrenodoxin-reductase (AdRed) and adrenodin (Adx) for
 CC the construction of P450sc-AdRed, P450sc-Adx-AdRed and
 CC P450sc-AdRed-Adx fusion enzymes capable of cholesterol disposal.
 CC AdRed cDNA is amplified using primers 5-8 (AAQ79880-83,
 CC respectively).
 XX
 SQ Sequence 34 BP; 4 A; 10 C; 16 G; 4 T; 0 other;
 XX

Query Match 60.0%; Score 13.8; DB 16; Length 34;
 Best Local Similarity 88.2%; Pred. No. 2.4e+03;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 6 gcgtctcgtgggcaca 22
 ||| ||| ||| ||| ||| |||
 Db 32 GCGCCTCTGGGCCACA 16

RESULT 8
 ID AAZ65685/C
 XX AAZ65685 standard; DNA; 47 BP.
 XX
 AC AAZ65685;
 XX
 XX
 DT 11-SEP-2001 (first entry)
 XX
 DE Human map-related biallelic marker SEQ ID NO:32.
 XX
 DE Human genome; biallelic marker; high density disequilibrium map;
 KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
 KW haplotyping; hybridisation; identification; characterisation;
 KW diagnosis; single nucleotide polymorphism; SNP; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT variation replace(24,C)
 FT /*tag= a
 FT /standard_name= "single nucleotide polymorphism"
 XX
 PN WO954500-A2.
 XX
 XX 28-OCT-1999.
 XX
 XX 21-APR-1999; 99WO-IB00822.
 XX
 XX 21-APR-1998; 98US-0082614.
 PR 23-NOV-1998; 98US-0109732.
 XX
 XX (GEST) GENSET.
 PA
 XX Cohen D, Blumenfeld M, Chumakov I;
 PI WPI; 2000-013267/01.
 XX
 XX Novel biallelic markers used to construct a high density disequilibrium
 PT map of the human genome
 XX
 XX Claim 1; Page 237; 2745pp; English.
 PS
 XX

CC AAZ65654 to AAZ69578 represent human biallelic markers from the present
 CC invention, which contain a polymorphic base at position 24 of their
 CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
 CC primers for the biallelic markers. The biallelic markers of the
 CC invention have a variety of uses: they can be used for high density
 CC mapping of the human genome, and in complex association studies and
 CC haplotyping studies which are useful in determining the genetic basis
 CC for disease states. Compositions and methods of the invention can also
 CC be useful for the identification of the targets for the development of
 CC pharmaceutical agents and diagnostic methods, as well as the
 CC characterisation of the differential efficacious responses to and side
 CC effects from pharmaceutical agents acting on a disease as well as other
 CC treatment.
 CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297
 CC and 3367, are not actually given a sequence in the Sequence Listing
 CC from the present invention.
 XX
 SQ Sequence 47 BP; 16 A; 10 C; 13 G; 8 T; 0 other;
 XX

Query Match 60.0%; Score 13.8; DB 21; Length 47;
 Best Local Similarity 88.2%; Pred. No. 2.5e+03;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 6 gcgtctcgtgggcaca 22
 ||| ||| ||| ||| ||| |||
 Db 28 GCTTCTCTGGGCCACA 12

RESULT 9
 ID AAQ58908
 XX AAQ58908 standard; DNA; 48 BP.
 XX
 AC AAQ58908;
 XX
 XX 26-OCT-1994 (first entry)
 DT
 XX
 DE E.coli beta-glucuronidase cloning oligonucleotide E.coli-B-Gluc.back.
 XX
 DE Carcinobryonic antigen; single chain variable region; sfv fragment;
 KW fusion gene; cancer treatment; targetted drug delivery; tumour;
 KW Escherichia coli; beta-glucuronidase; prodrug activating enzyme; ss.
 OS Synthetic.
 XX
 XX EP590530-A.
 PN
 XX 06-APR-1994.
 PD
 XX 24-SEP-1993; 93EP-0115418.
 PF
 XX 02-OCT-1992; 92DE-4233152.
 PR
 XX (BEHW) BEHRINGERWERKE AG.
 PA
 XX Bosslet K, Czech J, Gehrman M, Seemann G;
 PI WPI; 1994-111012/14.
 XX
 XX New fusion protein contg. enzyme for prodrug activation - coupled
 PT to antigen binding component, esp. sfv antibody fragment, partic.
 PT for treatment of tumours
 XX
 XX Example 10; Page 21; 35pp; German.
 PS
 XX Oligonucleotides E.coli-B-Gluc.for (AAQ58907) and E.coli-B-Gluc.back
 CC (AAQ58908) were used for cloning the E.coli beta-glucuronidase gene
 CC into a pUC19 vector all ready containing an anti-CEA single chain
 CC antibody construct sfv 431/26. The resultant fusion protein is useful
 CC for targetting beta-glucuronidase to cancer cells expressing CEA,
 CC where the enzyme is able to convert a prodrug into its active form.
 XX
 SQ Sequence 48 BP; 14 A; 14 C; 12 G; 8 T; 0 other;
 XX

```
Query Match      60.0%; Score 13.8; DB 15; Length 48;
Best Local Similarity 88.2%; Pred. No. 2.5e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 gcgtctcgtgggccaca 22
Db 13 gcgtctcgtgggccaca 29
      ||||| | |||||

RESULT 10
AAQ78241
ID AAQ78241 standard; DNA; 48 BP.
XX
AC AAQ78241;
XX
DT 13-JUL-1995 (first entry)
XX
DE Primer for amplifying E.coli beta glucuronidase gene.
XX
KW Humanised antibody; heavy chain; light chain; variable region;
KW beta-glucuronidase; linker; hinge region; single-chain; primer; ss.
XX
OS Synthetic.
XX
PN EP623352-A.
XX
PD 09-NOV-1994.
XX
PF 25-APR-1994; 94EP-0106394.
XX
PR 04-MAY-1993; 93DE-4314556.
XX
PA (BEHW ) BEHRINGERKE AG.
XX
PI Bosslet K, Czech J, Hoffmann D;
XX
DR WPI; 1994-343079/43.
XX
PT Bifunctional glycoproteins having a modified carbohydrate
PT complement - comprising a tumour-binding portion and an enzyme
PT which activates a prodrug to give a cytotoxic drug, for
PT tumour-selective therapy.
XX
PS Example 5; Page 12; 28pp; English.
XX
CC A humanised single-chain fusion protein from a humanised tumour
CC antibody moiety and human recombinant beta-glucuronidase was
CC recombinantly produced. The Vh gene, including its own signal
CC sequence, was amplified from pABstop 431/26 hum Vh using the
CC oligonucleotides pAB-Back (AAQ78236) and Linker-Anti (AAQ78237). The V1
CC gene was amplified from pABstop 431/26 hum V1 using the
CC oligonucleotides Linker-Sense (AAQ78238) and VL(Mut)-For
CC (AAQ78239). A PCR fragment was obtained which was composed of the Vh
CC gene connected to the V1 gene via a linker. The linker
CC oligonucleotides encode a polypeptide linker intended to link the
CC Vh and V1 domains to form a single-chain Fv (sfv) fragment. The
CC sfv fragment was ligated into pABstop 431/26VhhubetaqlucLH. The
CC plasmid clone pMCG-E1 contains the humanised sfv 431/26, a hinge
CC exon and the complete beta-glucuronidase. The humanised sfv
CC fragment was amplified with the primers pAB-Back (as above) and sfv
CC For (AAQ78240) and was ligated into pUC18 to give plasmid clone
CC pKB01. The gene encoding the Escherichia coli beta glucuronidase was
CC amplified from the vector pRAJ260 using the primers E.coli
CC Beta-gluc-Back 1 (This sequence) and E.coli beta-gluc-For (AAQ78242).
CC The resulting fragment was cloned into vector pKB01 to give pKB02
CC contg. sfv 431/26 linked to E.coli beta glucuronidase via a linker
CC sequence.
XX
SQ Sequence 48 BP; 14 A; 14 C; 12 G; 8 T; 0 other;

Query Match      60.0%; Score 13.8; DB 15; Length 48;
Best Local Similarity 88.2%; Pred. No. 2.5e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 gcgtctcgtgggccaca 22
Db 13 gcgtctcgtgggccaca 29
      ||||| | |||||

RESULT 11
AAT62433/C
ID AAT62433 standard; cDNA; 20 BP.
XX
AC AAT62433;
XX
DT 08-JUL-1997 (first entry)
XX
DE Bovine beta-mannosidosis carrier test antisense primer MJ-125.
XX
KW Bovine; beta-mannosidase; enzyme; kidney; affinity chromatography;
KW antibody; primer; probe; PCR; polymerase chain reaction; amplification;
KW thyroid; hybridisation; detection; point mutation; beta-mannosidosis;
KW cattle; carrier; Saler breed; ss.
XX
OS Synthetic.
XX
PN US5605797-A.
XX
PD 25-FEB-1997.
XX
PF 15-SEP-1994; 94US-0306546.
XX
PR 15-SEP-1994; 94US-0306546.
XX
PA (UNMS ) UNIV MICHIGAN STATE.
XX
PI Cavanagh KT, Chen H, Friderici K, Jones MZ;
XX
DR WPI; 1997-153571/14.
XX
PT Oligo:nucleotide fragments of bovine beta-mannosidase gene - for
PT detecting mutation associated with beta-mannosidosis
XX
PS Example 2; Column 18; 39pp; English.
XX
CC The primers AAT62432-3 were used to detect beta-mannosidosis carriers by
CC detecting a mutation in the beta-mannosidase gene (AAT62419). The
CC method of detection is artificial introduction of restriction site (AIRS)
CC which involves amplifying a 187 bp fragment of the genomic sequence
CC around the point mutation and selectively introducing a BstNI restriction
CC enzyme site, especially in the wild type sequence. The mutant sequence
CC will not contain this site after amplification. Thus upon restriction
CC digestion with BstNI, wild type and mutant sequences can be separated.
CC This primer corresponds to bases 2721-2740 of the bovine beta-mannosidase
CC gene sequence. The assays can be used to identify cattle that are
CC carriers of beta-mannosidosis, e.g. in the Saler breed.
XX
SQ Sequence 20 BP; 7 A; 5 C; 5 G; 3 T; 0 other;

Query Match      59.1%; Score 13.6; DB 18; Length 20;
Best Local Similarity 80.0%; Pred. No. 2.9e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 aggcgtctcgtgggccacat 23
Db 20 AGGTGTCFCGTAGCCACTT 1
      ||| ||||| |||||

RESULT 12
AAV64130/C
ID AAV64130 standard; DNA; 20 BP.
XX
```



```
AC AAV64130;
XX
DT 25-JAN-1999 (first entry)
XX
DE Bovine beta-mannosidase PCR antisense primer MJ-125.
XX
KW Bovine; beta-mannosidase; beta-mannosidosis; diagnosis; goat; cattle;
KW primary storage product; tremor; deafness; dysmyelination; PCR primer;
KW ss.
XX
OS Synthetic.
OS Bos taurus.
XX
XX US5837836-A.
XX
XX 17-NOV-1998.
XX
XX 19-SEP-1995; 95US-0530524.
XX
XX 15-SEP-1994; 94US-0306546.
XX
XX 19-SEP-1995; 95US-0530524.
XX
XX (UNMS ) UNIV MICHIGAN STATE.
XX
XX Cavanagh KT, Chen H, Friderici K, Jones WZ;
PI WPI; 1999-023539/02.
XX
XX Bovine beta-mannosidase nucleic acid sequence and mutation(s) -
XX useful for diagnosis of the disease beta-mannosidosis and its
XX carriers
XX
XX Example 2; Column 18; 39pp; English.
XX
XX The present sequence represents a PCR primer for bovine beta-mannosidase.
XX The present invention also describes a nucleic acid molecule encoding
XX bovine beta-mannosidase, but where the adenine at position 2648 is
XX replaced by guanine. The nucleic acid is useful for the detection of the
XX disease beta-mannosidosis. This is an autosomal recessive inherited
XX disorder affecting mainly goats and cattle, caused a defect in the
XX enzyme beta-mannosidase. This mutation renders the inflicted animals
XX incapable of correctly processing primary storage products, resulting in
XX tremors, deafness and dysmyelination amongst other symptoms. The nucleic
XX acid is used in hybridisation assays, or other nucleic acid based assays
XX (e.g. PCR or restriction mapping) to detect beta-mannosidase, especially
XX where nucleic acid encoding bovine beta-mannosidase contains the adenine
XX to guanine mutation at position 2648, for specific detection of the
XX disease. The nucleic acid allows specific detection of presence or
XX absence of the disease. Previous detection methods relied on enzyme
XX activity assays which can be inaccurate as the range of activities
XX greatly varies from one individual to another, especially when tested
XX for in cross-breeds.
XX
XX Sequence 20 BP; 7 A; 5 C; 5 G; 3 T; 0 other;
SQ

Query Match 59.1%; Score 13.6; DB 20; Length 20;
Best Local Similarity 80.0%; Pred. No. 2.9e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 aggcgtctcgtggccacat 23
DB 20 AGGTGTCGCTTAGCCACTT 1

RESULT 13
AAQ63451
ID AAQ63451 standard; DNA; 45 BP.
XX
XX AAQ63451;
XX
XX 18-NOV-1994 (first entry)
XX
```

```
DE REI human Ab L chain variable region synthetic fragment.
XX
XX Monoclonal antibody; Ab; ganglioside GM2; chimera;
KW chimeric antibody; expression vector; heavy; light; chain;
KW hypervariable region; CDR; constant region; hybridoma;
KW Ig; immunoglobulin; promoter; enhancer; ds.
XX
OS Synthetic.
XX
XX AU9346181-A.
XX
XX 17-MAR-1994.
XX
XX 07-SEP-1993; 93AU-0046181.
XX
XX 07-SEP-1992; 92JP-0238452.
XX
XX (KYOW ) KYOWA HAKKO KOGYO KK.
XX
XX Hanai N, Hasegawa M, Koike M, Kuwana Y, Nakamura K;
PI Shitara K;
XX
XX WPI; 1994-126857/16.
XX
XX Humanised antibody specific for ganglioside GM2 - used for
XX producing a cytotoxic effect on cancers such as melanoma,
XX neuroblastoma and glioma.
XX
XX Example 2; Page 121; 191pp; English.
XX
XX REI was used as human Ab L chain variable region-encoding
XX DNA to which CDRs were to be transplanted. DNAs given in
XX CC AAQ63448-53 were synthesised and ligated in order to obtain
XX CC a DNA, hKM796L (AAQ77823).
XX
XX Sequence 45 BP; 9 A; 14 C; 9 G; 13 T; 0 other;
SQ

Query Match 59.1%; Score 13.6; DB 15; Length 45;
Best Local Similarity 80.0%; Pred. No. 3e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 accaggcgtctcgtggccca 20
DB 25 acctggcttctggtgcca 44

RESULT 14
AAQ99493
ID AAX99493 standard; DNA; 45 BP.
XX
XX AAX99493;
XX
XX 04-NOV-1999 (first entry)
XX
XX Synthetic DNA for production of hKM796L, from REI.
XX
XX nucleotide; primer; immunoglobulin; light chain; plasmid;
KW REI; ds.
XX
XX Synthetic.
XX
XX Homo sapiens.
XX
XX US5939532-A.
XX
XX 17-AUG-1999.
XX
XX 07-JUN-1995; 95US-0483528.
XX
XX 07-JUN-1995; 95US-0483528.
XX
XX 07-SEP-1993; 93US-0116778.
XX
XX (KYOW ) KYOWA HAKKO KOGYO KK.
```

XX Hanai N, Hasegawa M, Koike M, Kuwana Y, Nakamura K;
PI Shitara K;
XX WPI; 1999-468416/39.
XX Chimeric human antibody expression vectors
PT Example 2; Column 105-107; 188pp; English.
XX This sequence can be used with sequences AAX99490 to AAX99495 to replace
CC part of the REI DNA, which is acting as a substitute immunoglobulin
CC heavy chain. The resulting DNA encodes for the human KM796 light chain.
CC The chimeric human antibodies are useful in the treatment of
CC cancer, especially that which is of neural ectodermal origin.
CC In contrast to prior art constructs based on mouse monoclonal
CC antibodies, the chimeric human antibodies do not cause
CC anti-mouse immunoglobulin production.
CC The chimeric human antibodies have a prolonged half-life and a
CC reduced frequency of adverse effects when compared to mouse monoclonal
CC antibodies.
XX Sequence 45 BP; 9 A; 14 C; 9 G; 13 T; 0 other;
SQ

Query Match 59.1%; Score 13.6; DB 20; Length 45;
Best Local Similarity 80.0%; Pred. No. 3e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 1 accaggcgctctcgtgggcca 20
||| ||| ||| ||| |||
Db 25 acctggctctcgtgtgcca 44

RESULT 15
AAV32874/C
ID AAV32874 standard; cDNA; 27 BP.
XX
AC AAV32874;
XX
DT 09-NOV-1998 (first entry)
XX
DE Human Borna disease virus p40 DNA 5' PCR primer.
XX
KW BDV; infection; diagnosis; neuropsychiatric disorder; human;
KW PCR; primer; ss.
XX
OS Synthetic.
OS Borna disease virus.
XX
FN W09830238-A1.
XX
PD 16-JUL-1998.
XX
PF 07-JAN-1998; 98WO-US00495.
XX
PR 07-JAN-1997; 97US-0779764.
XX
PA (SCRI) SCRIPPS RES INST.
XX
PI De La Torre JC;
XX
DR WPI; 1998-398802/34.
XX
XX New isolated human Borna disease nucleic acid(s) - which encode p24,
PT p16, p56, p40 and L polymerase catalytic domain polypeptide(s),
PT used to develop products for detection
XX
XX Example; Page 107; 207pp; English.
PS
XX This 5' primer is used with a 3' primer (see AAV32875) in the
CC PCR amplification of cDNA (see AAV32851-53) coding for the p40
CC polypeptide (see AAW49051-53) of human borna disease virus (BDV).

CC The PCR product is suitable for incorporation into a baculovirus
CC expression system, and recombinant polypeptide can be produced in
CC Spodoptera frugiperda Sf158 cells. Human BDV polypeptides,
CC polynucleotides and antibodies are used in claimed methods for
CC detecting human BDV or human BDV-like viral infection,
CC particularly in patients with neuropsychiatric disorders.
XX
SQ Sequence 27 BP; 6 A; 8 C; 8 G; 5 T; 0 other;

Query Match 58.3%; Score 13.4; DB 19; Length 27;
Best Local Similarity 73.9%; Pred. No. 3.7e+03;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy 1 accaggcgctctcgtgggcca 23
| ||||| ||| |||
Db 23 ATCAGGCGTCTCCCGGGTGGCAT 1

Search completed: August 17, 2002, 23:28:35
Job time: 4115 sec

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OM nucleic - nucleic search, using sw model

Run on: August 17, 2002, 22:16:15 ; Search time 45.56 Seconds
(without alignments)
124.003 Million cell upd

Title: US-09-700-906A-3

Perfect score: 23

Sequence: 1 accaggcgtctcgtgqccacat 23

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 543772

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Maximum DB seq length: 50
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

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4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PTCUS_COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %		Length	DB	ID	Description
		Match					
1	14.6	63.5	23	1	US-08-624-545-66	Sequence 66, Appl	
C 2	14.2	61.7	30	4	US-09-242-690A-20	Sequence 20, Appl	
C 3	13.8	60.0	34	1	US-08-075-193-16	Sequence 16, Appl	
C 4	13.8	60.0	34	2	US-08-564-090A-16	Sequence 16, Appl	
C 5	13.8	60.0	34	5	PCT-US94-06698-16	Sequence 16, Appl	
C 6	13.6	59.1	20	1	US-08-306-546C-4	Sequence 4, Appl	
C 7	13.6	59.1	20	2	US-08-530-524A-4	Sequence 4, Appl	
C 8	13.6	59.1	45	1	US-07-946-421-36	Sequence 36, Appl	
C 9	13.6	59.1	45	1	US-08-459-310-6	Sequence 6, Appl	
10	13.6	59.1	45	2	US-08-116-778E-33	Sequence 33, Appl	
11	13.6	59.1	45	2	US-08-438-563-33	Sequence 33, Appl	
12	13.6	59.1	45	2	US-08-483-528B-33	Sequence 33, Appl	
13	13.6	59.1	45	3	US-08-673-799C-33	Sequence 33, Appl	
C 14	13.4	58.3	27	3	US-08-779-764A-60	Sequence 60, Appl	
C 15	13.4	58.3	42	2	US-08-930-274-5	Sequence 5, Appl	
C 16	12.6	54.8	27	1	US-08-343-785-13	Sequence 13, Appl	
C 17	12.6	54.8	27	2	US-08-462-221-13	Sequence 13, Appl	
C 18	12.6	54.8	27	3	US-08-946-458-13	Sequence 13, Appl	
C 19	12.6	54.8	34	2	US-08-483-528B-43	Sequence 43, Appl	
C 20	12.6	54.8	34	3	US-08-836-561-21	Sequence 21, Appl	
C 21	12.6	54.8	34	3	US-08-673-799C-43	Sequence 43, Appl	
C 22	12.6	54.8	35	1	US-08-458-067-36	Sequence 36, Appl	
C 23	12.6	54.8	35	5	PCT-US96-07795-36	Sequence 36, Appl	
C 24	12.6	54.8	35	5	PCT-US96-07796-36	Sequence 36, Appl	
C 25	12.4	53.9	25	4	US-09-306-405-61	Sequence 61, Appl	
26	12.4	53.9	29	1	US-08-712-241-15	Sequence 15, Appl	
27	12.4	53.9	37	4	US-09-600-747-4	Sequence 4, Appl	

101	11.6	50.4	50	2	US-08-488-402A-73	Sequence 73, Appl	174	11	47.8	32	4	US-08-897-333A-8	Sequence 8, Appl1
102	11.6	50.4	50	2	US-08-484-552A-73	Sequence 73, Appl	175	11	47.8	33	1	US-08-438-639-38	Sequence 38, Appl1
103	11.6	50.4	50	5	PCT-US96-09472-73	Sequence 73, Appl	176	11	47.8	33	1	US-07-813-338A-38	Sequence 38, Appl1
c 104	11.4	49.6	21	3	US-08-985-090-21	Sequence 21, Appl	177	11	47.8	33	3	US-08-441-971-113	Sequence 113, App
c 105	11.4	49.6	17	3	US-09-165-543-22	Sequence 22, Appl	c 178	11	47.8	33	4	US-08-897-333A-7	Sequence 7, Appl1
106	11.4	49.6	22	4	US-09-475-316A-81	Sequence 81, Appl	179	11	47.8	33	4	US-08-221-653-113	Sequence 113, App
107	11.4	49.6	22	4	US-08-881-189B-9	Sequence 9, Appl	180	11	47.8	33	4	US-08-442-144A-113	Sequence 113, App
c 108	11.4	49.6	26	2	US-08-859-998-1276	Sequence 9, Appl	181	11	47.8	33	4	US-08-441-570-113	Sequence 113, App
c 109	11.4	49.6	26	4	US-09-225-928-1276	Sequence 1276, Ap	182	11	47.8	34	4	US-09-155-078-3	Sequence 3, Appl1
c 110	11.4	49.6	27	1	US-08-712-241-16	Sequence 16, Appl	183	11	47.8	35	1	US-08-384-489-35	Sequence 35, Appl
c 111	11.4	49.6	27	3	US-08-513-974B-70	Sequence 70, Appl	184	11	47.8	35	1	US-08-384-489-37	Sequence 37, Appl
c 112	11.4	49.6	28	4	US-08-881-189B-19	Sequence 19, Appl	185	11	47.8	36	5	PCT-US94-09700-23	Sequence 23, Appl
c 113	11.4	49.6	30	1	US-08-483-743-5	Sequence 5, Appl	186	11	47.8	37	4	US-09-450-072-41	Sequence 41, Appl
c 114	11.4	49.6	30	1	US-08-483-743-5	Sequence 5, Appl	187	11	47.8	40	2	US-08-963-946-6	Sequence 6, Appl
c 115	11.4	49.6	30	1	US-08-474-624-5	Sequence 5, Appl	188	11	47.8	41	2	US-08-963-946-5	Sequence 5, Appl
c 116	11.4	49.6	30	1	US-08-474-624-6	Sequence 6, Appl	189	11	47.8	48	1	US-08-137-17D-81	Sequence 81, Appl
c 117	11.4	49.6	30	3	US-08-803-085-15	Sequence 15, Appl	190	11	47.8	48	1	US-08-436-717-81	Sequence 81, Appl
c 118	11.4	49.6	31	3	US-09-200-232-3	Sequence 3, Appl	191	10.8	47.0	20	1	US-07-940-242A-80	Sequence 80, Appl
c 119	11.4	49.6	31	3	US-09-219-932-6	Sequence 6, Appl	192	10.8	47.0	21	4	US-08-050-482A-7	Sequence 7, Appl1
c 120	11.4	49.6	32	1	US-08-912-976-9	Sequence 9, Appl	193	10.8	47.0	24	2	US-08-851-135-10	Sequence 10, Appl
c 121	11.4	49.6	32	4	US-08-844-045C-6	Sequence 6, Appl	194	10.8	47.0	24	2	US-08-787-902A-4	Sequence 4, Appl
c 122	11.4	49.6	32	4	US-09-476-299-29	Sequence 29, Appl	195	10.8	47.0	24	4	US-09-344-700-14	Sequence 14, Appl
c 123	11.4	49.6	36	2	US-09-609-154-29	Sequence 29, Appl	196	10.8	47.0	24	4	US-09-450-672-25	Sequence 25, Appl
c 124	11.4	49.6	36	2	US-08-432-071B-9	Sequence 9, Appl	197	10.8	47.0	25	4	US-09-098-628-65	Sequence 65, Appl
c 125	11.4	49.6	36	4	US-09-275-850-156	Sequence 156, App	198	10.8	47.0	25	4	US-09-546-250-6	Sequence 6, Appl1
c 126	11.4	49.6	36	5	PCT-US96-06075-5	Sequence 5, Appl	199	10.8	47.0	26	2	US-08-483-528B-42	Sequence 42, Appl
c 127	11.4	49.6	41	3	US-09-167-354-4	Sequence 4, Appl	c 200	10.8	47.0	26	2	US-08-859-998-376	Sequence 376, App
c 128	11.4	49.6	44	4	US-09-199-290-24	Sequence 24, Appl	c 201	10.8	47.0	26	2	US-08-836-561-20	Sequence 20, Appl
c 129	11.4	49.6	49	3	US-09-046-247-16	Sequence 16, Appl	2	10.8	47.0	26	3	US-08-673-799C-42	Sequence 42, Appl
c 130	11.2	48.7	18	2	US-08-486-969-50	Sequence 50, Appl	c 202	10.8	47.0	26	4	US-09-225-928-376	Sequence 376, App
c 131	11.2	48.7	18	2	US-08-857-946-23	Sequence 23, Appl	c 203	10.8	47.0	26	4	US-09-338-992B-7	Sequence 7, Appl1
c 132	11.2	48.7	18	3	US-08-970-740-23	Sequence 23, Appl	204	10.8	47.0	27	1	PCT-US95-09057-7	Sequence 7, Appl1
c 133	11.2	48.7	18	3	US-09-280-409-57	Sequence 57, Appl	205	10.8	47.0	27	5	PCT-US95-09057-7	Sequence 7, Appl1
c 134	11.2	48.7	18	3	US-09-280-409-52	Sequence 92, Appl	c 206	10.8	47.0	28	1	US-08-292-081A-2	Sequence 2, Appl1
c 135	11.2	48.7	22	1	US-08-531-747-8	Sequence 8, Appl	c 207	10.8	47.0	28	2	US-08-752-495-2	Sequence 2, Appl1
c 136	11.2	48.7	22	1	US-08-531-749-8	Sequence 8, Appl	208	10.8	47.0	29	2	US-08-467-603-31	Sequence 31, Appl
c 137	11.2	48.7	22	1	US-08-781-432-8	Sequence 8, Appl	209	10.8	47.0	29	2	US-08-466-793-31	Sequence 31, Appl
c 138	11.2	48.7	22	2	US-08-859-998-1247	Sequence 1247, Ap	c 210	10.8	47.0	29	2	US-07-832-905B-29	Sequence 29, Appl
c 139	11.2	48.7	23	2	US-09-225-928-1247	Sequence 1247, Ap	c 211	10.8	47.0	30	1	US-08-153-848-58	Sequence 58, Appl
c 140	11.2	48.7	23	4	US-09-067-626-6	Sequence 6, Appl	c 212	10.8	47.0	30	1	US-08-153-848-59	Sequence 59, Appl
141	11.2	48.7	25	4	US-09-672-609-34	Sequence 34, Appl	c 213	10.8	47.0	30	1	US-08-700-757-29	Sequence 29, Appl
142	11.2	48.7	31	2	US-08-841-483-11	Sequence 11, Appl	c 214	10.8	47.0	30	2	US-08-821-782-27	Sequence 27, Appl
143	11.2	48.7	31	4	US-09-382-911-11	Sequence 11, Appl	c 215	10.8	47.0	30	2	US-09-239-843A-58	Sequence 58, Appl
144	11.2	48.7	38	2	US-08-713-941-10	Sequence 10, Appl	c 216	10.8	47.0	30	3	US-09-299-843A-59	Sequence 59, Appl
145	11.2	48.7	39	1	US-08-199-507B-29	Sequence 29, Appl	c 217	10.8	47.0	30	4	US-09-084-120-8	Sequence 8, Appl1
146	11.2	48.7	39	1	US-08-199-507B-51	Sequence 51, Appl	c 218	10.8	47.0	30	4	US-09-292-435A-27	Sequence 27, Appl
147	11.2	48.7	39	1	US-08-441-828-29	Sequence 29, Appl	c 219	10.8	47.0	30	4	US-09-088-337B-58	Sequence 58, Appl
148	11.2	48.7	39	1	US-08-441-828-51	Sequence 51, Appl	c 220	10.8	47.0	30	4	US-09-088-337B-59	Sequence 59, Appl
149	11.2	48.7	40	1	US-08-199-507B-45	Sequence 45, Appl	c 221	10.8	47.0	30	4	PCT-US93-11153-58	Sequence 58, Appl
150	11.2	48.7	40	1	US-08-199-507B-50	Sequence 50, Appl	c 222	10.8	47.0	30	5	PCT-US93-11153-59	Sequence 59, Appl
151	11.2	48.7	40	1	US-08-441-828-45	Sequence 45, Appl	c 223	10.8	47.0	31	1	US-08-114-859-2	Sequence 2, Appl1
152	11.2	48.7	40	1	US-08-441-828-50	Sequence 50, Appl	c 224	10.8	47.0	31	2	US-08-858-623A-20	Sequence 20, Appl
153	11.2	48.7	43	3	US-08-874-825-48	Sequence 48, Appl	c 225	10.8	47.0	31	2	US-08-858-623A-9	Sequence 9, Appl1
154	11.2	48.7	43	3	US-08-663-824-48	Sequence 48, Appl	c 226	10.8	47.0	33	2	US-09-178-089-2	Sequence 2, Appl1
155	11.2	48.7	49	2	US-08-450-370A-2	Sequence 2, Appl	c 227	10.8	47.0	35	3	US-09-178-089-2	Sequence 2, Appl1
c 156	11	47.8	19	4	US-09-226-012-56	Sequence 56, Appl	c 228	10.8	47.0	39	1	US-08-418-123A-20	Sequence 20, Appl
c 157	11	47.8	23	2	US-08-461-286-5	Sequence 5, Appl	c 229	10.8	47.0	39	2	US-08-938-858-10	Sequence 10, Appl
158	11	47.8	23	5	PCT-US92-02854-5	Sequence 5, Appl	c 230	10.8	47.0	39	3	US-08-963-927-10	Sequence 10, Appl
159	11	47.8	26	1	US-08-467-607-20	Sequence 20, Appl	c 231	10.8	47.0	39	4	US-09-481-810-10	Sequence 10, Appl
160	11	47.8	26	2	US-08-469-362-20	Sequence 20, Appl	c 232	10.8	47.0	40	1	US-08-458-067-17	Sequence 17, Appl
161	11	47.8	26	2	US-08-850-392-20	Sequence 20, Appl	c 233	10.8	47.0	40	4	US-09-171-945-129	Sequence 129, App
162	11	47.8	27	1	US-08-264-861A-9	Sequence 9, Appl	c 234	10.8	47.0	40	5	PCT-US96-07795-17	Sequence 17, Appl
163	11	47.8	27	1	US-08-478-039-29	Sequence 29, Appl	c 235	10.8	47.0	40	5	PCT-US96-07796-17	Sequence 17, Appl
164	11	47.8	27	1	US-08-149-099C-7	Sequence 7, Appl	c 236	10.8	47.0	42	3	US-08-874-825-12	Sequence 12, Appl
165	11	47.8	27	1	US-08-476-349A-29	Sequence 29, Appl	c 237	10.8	47.0	42	3	US-08-663-824-12	Sequence 12, Appl
166	11	47.8	27	1	US-08-476-275-10	Sequence 10, Appl	c 238	10.8	47.0	44	2	US-08-962-232-2	Sequence 2, Appl1
167	11	47.8	27	2	US-08-478-967A-7	Sequence 7, Appl	c 239	10.8	47.0	45	1	US-07-834-539A-59	Sequence 59, Appl
168	11	47.8	27	3	US-08-523-894-22	Sequence 22, Appl	c 240	10.8	47.0	45	1	US-07-834-539A-60	Sequence 60, Appl
169	11	47.8	30	5	PCT-US95-07784-9	Sequence 9, Appl	c 241	10.8	47.0	45	1	US-08-053-131-107	Sequence 107, App
c 170	11	47.8	30	2	US-08-475-000-3	Sequence 3, Appl	c 242	10.8	47.0	45	1	US-08-053-131-108	Sequence 108, App
c 171	11	47.8	30	2	US-08-483-199-3	Sequence 3, Appl	c 243	10.8	47.0	45	1	US-08-645-641-107	Sequence 107, App
c 172	11	47.8	31	3	US-08-484-508-3	Sequence 3, Appl	c 244	10.8	47.0	45	1	US-08-645-641-108	Sequence 108, App
c 173	11	47.8	31	3	US-09-123-345-3	Sequence 3, Appl	c 245	10.8	47.0	45	1	US-07-853-408B-107	Sequence 107, App
c 174	11	47.8	31	3	US-09-123-345-3	Sequence 3, Appl	c 246	10.8	47.0	45	1	US-07-853-408B-108	Sequence 108, App

247	10.8	47.0	45	1	US-08-096-762-107	Sequence 107, App	320	10.6	46.1	27	1	US-08-035-634-13	Sequence 13, Appl
c 248	10.8	47.0	45	1	US-08-096-762-108	Sequence 108, App	321	10.6	46.1	27	1	US-08-682-073-5	Sequence 5, Appli
249	10.8	47.0	45	2	US-08-800-353-59	Sequence 59, Appl	c 322	10.6	46.1	27	1	US-08-487-037-6	Sequence 6, Appli
c 250	10.8	47.0	45	2	US-08-800-353-60	Sequence 60, Appl	323	10.6	46.1	27	2	US-09-254-325-8	Sequence 8, Appli
c 251	10.8	47.0	45	2	US-08-308-865-107	Sequence 107, App	324	10.6	46.1	32	2	US-08-737-271-2	Sequence 2, Appli
c 252	10.8	47.0	45	2	US-08-308-865-108	Sequence 108, App	325	10.6	46.1	32	3	US-09-058-555-2	Sequence 2, Appli
c 253	10.8	47.0	45	2	US-08-982-232-1	Sequence 1, Appli	326	10.6	46.1	33	3	US-08-470-124-64	Sequence 64, Appl
c 254	10.8	47.0	45	3	US-08-863-813A-56	Sequence 56, Appl	327	10.6	46.1	33	3	US-08-441-971-130	Sequence 130, App
c 255	10.8	47.0	45	4	US-09-042-353-300	Sequence 300, App	328	10.6	46.1	33	4	US-08-221-653-130	Sequence 130, App
c 256	10.8	47.0	45	4	US-09-042-353-301	Sequence 301, App	329	10.6	46.1	33	4	US-08-442-144A-130	Sequence 130, App
c 257	10.8	47.0	45	4	US-08-758-417A-148	Sequence 148, App	330	10.6	46.1	33	4	US-08-441-970-130	Sequence 130, App
c 258	10.8	47.0	45	4	US-08-758-417A-149	Sequence 149, App	331	10.6	46.1	35	1	US-08-912-976-26	Sequence 26, Appl
c 259	10.8	47.0	45	5	PCT-US92-06185-59	Sequence 59, Appl	332	10.6	46.1	36	1	US-08-608-584-1	Sequence 1, Appli
c 260	10.8	47.0	45	5	PCT-US92-06185-60	Sequence 60, Appl	333	10.6	46.1	36	2	US-08-889-909A-18	Sequence 18, Appl
c 261	10.8	47.0	45	5	PCT-US92-10983-107	Sequence 107, App	334	10.6	46.1	36	4	US-09-156-163A-18	Sequence 18, Appl
c 262	10.8	47.0	45	5	PCT-US92-10983-108	Sequence 108, App	c 335	10.6	46.1	37	4	US-07-875-790B-10	Sequence 10, Appl
c 263	10.8	47.0	46	1	US-08-403-762A-14	Sequence 14, Appl	336	10.6	46.1	38	1	US-08-182-114-3	Sequence 3, Appli
c 264	10.8	47.0	46	1	US-08-661-507-4	Sequence 4, Appli	337	10.6	46.1	39	1	US-08-608-584-4	Sequence 4, Appli
c 265	10.8	47.0	46	2	US-08-855-085-3	Sequence 3, Appli	338	10.6	46.1	39	1	US-08-682-218-23	Sequence 23, Appl
c 266	10.8	47.0	46	2	US-09-186-030-3	Sequence 3, Appli	339	10.6	46.1	40	1	US-08-682-218-23	Sequence 23, Appl
c 267	10.8	47.0	46	2	US-08-865-675-3	Sequence 3, Appli	340	10.6	46.1	40	3	US-08-949-770-3	Sequence 3, Appli
c 268	10.8	47.0	46	2	US-08-933-749-4	Sequence 4, Appli	341	10.6	46.1	40	3	US-08-875-944B-4	Sequence 4, Appli
c 269	10.8	47.0	46	2	US-09-237-510-3	Sequence 3, Appli	c 342	10.6	46.1	40	4	US-09-416-050A-33	Sequence 33, Appl
c 270	10.8	47.0	46	3	US-09-120-916-3	Sequence 3, Appli	c 343	10.6	46.1	40	4	US-09-416-050A-46	Sequence 46, Appl
c 271	10.8	47.0	46	3	US-08-964-020-7	Sequence 7, Appli	c 344	10.6	46.1	40	4	US-09-664-800-33	Sequence 33, Appl
c 272	10.8	47.0	46	3	US-09-235-583-4	Sequence 4, Appli	c 345	10.6	46.1	40	4	US-09-664-800-46	Sequence 46, Appl
c 273	10.8	47.0	46	4	US-09-599-164-4	Sequence 4, Appli	c 346	10.6	46.1	40	4	US-09-665-309-33	Sequence 33, Appl
c 274	10.8	47.0	48	1	US-08-292-081A-9	Sequence 9, Appli	c 347	10.6	46.1	40	4	US-09-665-309-46	Sequence 46, Appl
c 275	10.8	47.0	48	2	US-08-752-495-9	Sequence 9, Appli	c 348	10.6	46.1	40	4	US-09-661-569-33	Sequence 33, Appl
c 276	10.8	47.0	50	1	US-08-171-389-379	Sequence 379, App	c 349	10.6	46.1	40	4	US-09-661-569-46	Sequence 46, Appl
c 277	10.8	47.0	50	1	US-08-123-936-379	Sequence 379, App	350	10.6	46.1	42	4	US-09-290-577-32	Sequence 32, Appl
c 278	10.8	47.0	50	2	US-08-475-228A-379	Sequence 379, App	351	10.6	46.1	42	4	US-09-290-452-32	Sequence 32, Appl
c 279	10.8	47.0	50	3	US-08-482-080A-379	Sequence 379, App	352	10.6	46.1	42	4	US-09-290-338-32	Sequence 32, Appl
c 280	10.8	47.0	50	5	PCT-US93-12388-379	Sequence 379, App	c 353	10.6	46.1	43	4	US-09-439-897-40	Sequence 40, Appl
c 281	10.6	46.1	18	1	US-08-271-948A-55	Sequence 55, Appl	c 354	10.6	46.1	45	1	US-08-050-058B-29	Sequence 29, Appl
c 282	10.6	46.1	18	1	US-08-271-948A-55	Sequence 55, Appl	c 355	10.6	46.1	45	1	US-08-463-587A-29	Sequence 29, Appl
c 283	10.6	46.1	18	2	US-08-410-654B-32	Sequence 32, Appl	c 356	10.6	46.1	45	2	US-08-463-667A-33	Sequence 33, Appl
c 284	10.6	46.1	18	2	US-08-474-851-32	Sequence 32, Appl	c 357	10.6	46.1	45	2	US-08-441-871-85	Sequence 85, Appl
c 285	10.6	46.1	18	2	US-08-481-560-32	Sequence 32, Appl	c 358	10.6	46.1	45	3	US-08-923-854-29	Sequence 29, Appl
c 286	10.6	46.1	18	3	US-08-779-916A-55	Sequence 55, Appl	c 359	10.6	46.1	45	3	US-08-388-029A-96	Sequence 96, Appl
c 287	10.6	46.1	18	4	US-08-750-232-55	Sequence 55, Appl	c 360	10.6	46.1	45	3	US-08-863-813A-59	Sequence 59, Appl
c 288	10.6	46.1	18	5	PCT-US95-08604-55	Sequence 55, Appl	c 361	10.6	46.1	45	4	US-08-918-148-63	Sequence 63, Appl
c 289	10.6	46.1	18	5	PCT-US95-08606-55	Sequence 55, Appl	c 362	10.6	46.1	45	6	5244792-15	Patent No. 5244792
c 290	10.6	46.1	19	4	US-09-502-966-9	Sequence 9, Appli	c 363	10.6	46.1	46	1	US-08-171-389-144	Sequence 144, App
c 291	10.6	46.1	20	1	US-07-940-242A-8	Sequence 8, Appli	c 364	10.6	46.1	46	1	US-08-123-936-144	Sequence 144, App
c 292	10.6	46.1	20	1	US-08-557-139-30	Sequence 30, Appl	c 365	10.6	46.1	46	2	US-08-475-228A-144	Sequence 144, App
c 293	10.6	46.1	20	4	US-09-435-296-60	Sequence 60, Appl	c 366	10.6	46.1	46	3	US-08-482-080A-144	Sequence 144, App
c 294	10.6	46.1	20	4	US-09-490-692-59	Sequence 59, Appl	c 367	10.6	46.1	46	5	PCT-US93-12388-144	Sequence 144, App
c 295	10.6	46.1	20	4	US-08-268-710-3	Sequence 3, Appli	c 368	10.6	46.1	47	1	US-08-293-086-7	Sequence 7, Appli
c 296	10.6	46.1	21	2	US-08-793-229-6	Sequence 6, Appli	c 369	10.6	46.1	47	1	US-08-244-993-7	Sequence 7, Appli
c 297	10.6	46.1	21	3	US-09-285-957-6	Sequence 6, Appli	c 370	10.6	46.1	47	2	US-08-861-306-7	Sequence 7, Appli
c 298	10.6	46.1	22	1	US-07-884-811-6	Sequence 6, Appli	c 371	10.6	46.1	47	2	US-08-468-037A-34	Sequence 34, Appl
c 299	10.6	46.1	22	1	US-07-885-971-6	Sequence 6, Appli	c 372	10.6	46.1	47	2	US-08-471-973A-34	Sequence 34, Appl
c 300	10.6	46.1	22	1	US-08-087-783A-6	Sequence 6, Appli	c 373	10.6	46.1	47	2	US-08-465-880-15	Sequence 15, Appl
c 301	10.6	46.1	22	1	US-08-194-088B-6	Sequence 6, Appli	c 374	10.6	46.1	47	3	US-09-035-357-34	Sequence 34, Appl
c 302	10.6	46.1	22	1	US-08-435-501-5	Sequence 5, Appli	c 375	10.6	46.1	47	3	US-09-016-520-16	Sequence 16, Appl
c 303	10.6	46.1	22	1	US-08-599-253-53	Sequence 53, Appl	c 376	10.6	46.1	47	3	US-09-144-611-7	Sequence 7, Appli
c 304	10.6	46.1	22	1	US-08-435-764-5	Sequence 5, Appli	c 377	10.6	46.1	47	4	US-09-130-973-16	Sequence 16, Appl
c 305	10.6	46.1	22	1	US-08-792-078-5	Sequence 5, Appli	c 378	10.6	46.1	47	4	US-09-477-902-16	Sequence 16, Appl
c 306	10.6	46.1	22	2	US-08-194-087-6	Sequence 6, Appli	c 379	10.6	46.1	47	4	US-09-502-966-13	Sequence 13, Appl
c 307	10.6	46.1	22	5	PCT-US93-04648-6	Sequence 6, Appli	c 380	10.6	46.1	47	4	US-09-453-514A-7	Sequence 7, Appli
c 308	10.6	46.1	22	5	PCT-US93-04717-5	Sequence 5, Appli	c 381	10.6	46.1	49	1	US-08-429-181-34	Sequence 34, Appl
c 309	10.6	46.1	22	5	PCT-US96-06352-53	Sequence 53, Appl	382	10.6	46.1	49	1	US-08-164-388-34	Sequence 34, Appl
c 310	10.6	46.1	22	5	PCT-US96-06583-53	Sequence 53, Appl	c 383	10.6	46.1	49	2	US-08-652-558-21	Sequence 21, Appl
c 311	10.6	46.1	23	1	US-08-343-785-15	Sequence 15, Appl	c 384	10.4	45.2	13	3	US-08-882-046-78	Sequence 78, Appl
c 312	10.6	46.1	23	2	US-08-462-221-15	Sequence 15, Appl	c 385	10.4	45.2	15	1	US-08-182-968A-179	Sequence 179, App
c 313	10.6	46.1	23	3	US-08-793-229-5	Sequence 5, Appli	c 386	10.4	45.2	15	2	US-08-774-306A-179	Sequence 179, App
c 314	10.6	46.1	23	3	US-09-285-957-5	Sequence 5, Appli	c 387	10.4	45.2	15	3	US-09-064-156A-179	Sequence 179, App
c 315	10.6	46.1	23	3	US-08-946-458-15	Sequence 15, Appl	c 388	10.4	45.2	15	4	US-09-180-437-147	Sequence 147, App
c 316	10.6	46.1	25	1	US-08-343-785-14	Sequence 14, Appl	389	10.4	45.2	18	1	US-08-458-568A-12	Sequence 12, Appl
c 317	10.6	46.1	25	2	US-08-462-221-14	Sequence 14, Appl	390	10.4	45.2	19	3	US-08-840-551-4	Sequence 4, Appli
c 318	10.6	46.1	25	3	US-08-946-458-14	Sequence 14, Appl	391	10.4	45.2	20	1	US-07-952-442-10	Sequence 10, Appl
c 319	10.6	46.1	26	3	US-08-648-272-20	Sequence 20, Appl	392	10.4	45.2	20	1	US-08-269-766-10	Sequence 10, Appl

539	10.4	45.2	48	3	US-08-874-825-5	Sequence 5, Appl1	612	10.2	44.3	24	3	US-08-976-255-33	Sequence 33, Appl1
540	10.4	45.2	48	3	US-09-041-780-15	Sequence 15, Appl1	613	10.2	44.3	24	4	US-08-475-470A-16	Sequence 16, Appl1
541	10.4	45.2	48	3	US-08-335-844A-64	Sequence 64, Appl1	614	10.2	44.3	24	4	US-09-225-928-695	Sequence 695, Appl1
542	10.4	45.2	48	3	US-08-487-077A-9	Sequence 9, Appl1	c 615	10.2	44.3	24	5	PCT-US95-0409A-13	Sequence 13, Appl1
543	10.4	45.2	48	3	US-08-663-824-5	Sequence 5, Appl1	c 616	10.2	44.3	24	5	PCT-US95-04228-37	Sequence 37, Appl1
544	10.4	45.2	48	3	US-08-485-863A-9	Sequence 9, Appl1	c 617	10.2	44.3	25	1	US-08-182-961B-14	Sequence 14, Appl1
545	10.4	45.2	48	4	US-08-485-049D-9	Sequence 9, Appl1	618	10.2	44.3	25	3	US-08-513-974B-1	Sequence 1, Appl1
546	10.4	45.2	48	4	US-09-191-136-7	Sequence 7, Appl1	619	10.2	44.3	25	4	US-08-776-971-29	Sequence 29, Appl1
547	10.4	45.2	48	4	US-09-191-608-6	Sequence 6, Appl1	620	10.2	44.3	25	4	US-09-007-678B-14	Sequence 14, Appl1
548	10.4	45.2	48	4	US-09-264-693-3	Sequence 3, Appl1	621	10.2	44.3	26	1	US-08-288-728-20	Sequence 20, Appl1
549	10.4	45.2	48	4	US-09-178-115-9	Sequence 9, Appl1	622	10.2	44.3	26	1	US-08-330-535A-29	Sequence 29, Appl1
550	10.4	45.2	48	4	US-09-177-776-9	Sequence 9, Appl1	623	10.2	44.3	26	1	US-08-688-145-13	Sequence 13, Appl1
551	10.4	45.2	49	1	US-08-055-390-9	Sequence 9, Appl1	624	10.2	44.3	26	2	US-08-838-844-29	Sequence 29, Appl1
552	10.4	45.2	50	1	US-08-171-389-112	Sequence 112, App	c 625	10.2	44.3	27	1	US-07-988-194A-31	Sequence 31, Appl1
553	10.4	45.2	50	1	US-08-171-389-138	Sequence 138, App	626	10.2	44.3	27	2	US-08-726-012B-17	Sequence 17, Appl1
554	10.4	45.2	50	1	US-08-123-936-112	Sequence 112, App	627	10.2	44.3	27	4	US-09-253-396A-121	Sequence 121, App
555	10.4	45.2	50	1	US-08-123-936-138	Sequence 138, App	c 628	10.2	44.3	27	4	US-08-479-737-31	Sequence 31, Appl1
556	10.4	45.2	50	2	US-08-475-228A-112	Sequence 112, App	c 629	10.2	44.3	28	1	US-08-394-033-3	Sequence 3, Appl1
557	10.4	45.2	50	2	US-08-475-228A-138	Sequence 138, App	c 630	10.2	44.3	28	2	US-08-463-081B-19	Sequence 19, Appl1
558	10.4	45.2	50	2	US-08-479-733A-5	Sequence 5, Appl1	631	10.2	44.3	28	2	US-08-463-081B-20	Sequence 20, Appl1
559	10.4	45.2	50	2	US-08-479-733A-7	Sequence 7, Appl1	c 632	10.2	44.3	28	2	US-08-461-379A-19	Sequence 19, Appl1
560	10.4	45.2	50	2	US-08-479-733A-12	Sequence 12, Appl1	633	10.2	44.3	28	2	US-08-461-379A-20	Sequence 20, Appl1
561	10.4	45.2	50	2	US-08-479-733A-16	Sequence 16, Appl1	c 634	10.2	44.3	28	2	US-08-462-390B-19	Sequence 19, Appl1
562	10.4	45.2	50	3	US-08-487-427-5	Sequence 5, Appl1	635	10.2	44.3	28	2	US-08-462-390B-20	Sequence 20, Appl1
563	10.4	45.2	50	3	US-08-487-427-7	Sequence 7, Appl1	c 636	10.2	44.3	28	3	US-08-463-074B-19	Sequence 19, Appl1
564	10.4	45.2	50	3	US-08-487-427-12	Sequence 12, Appl1	637	10.2	44.3	28	3	US-08-463-074B-20	Sequence 20, Appl1
565	10.4	45.2	50	3	US-08-487-427-16	Sequence 16, Appl1	c 638	10.2	44.3	28	3	US-08-465-585C-19	Sequence 19, Appl1
566	10.4	45.2	50	3	US-08-482-080A-112	Sequence 112, App	639	10.2	44.3	28	3	US-08-465-585C-20	Sequence 20, Appl1
567	10.4	45.2	50	3	US-08-482-080A-138	Sequence 138, App	c 640	10.2	44.3	28	3	US-08-652-446-19	Sequence 19, Appl1
568	10.4	45.2	50	3	US-08-479-727A-5	Sequence 5, Appl1	641	10.2	44.3	28	3	US-08-652-446-20	Sequence 20, Appl1
569	10.4	45.2	50	3	US-08-479-727A-7	Sequence 7, Appl1	c 642	10.2	44.3	28	6	5256770-36	Patent No. 5256770
570	10.4	45.2	50	3	US-08-479-727A-12	Sequence 12, Appl1	643	10.2	44.3	29	3	US-09-126-280-16	Sequence 16, Appl1
571	10.4	45.2	50	3	US-08-479-727A-16	Sequence 16, Appl1	644	10.2	44.3	29	4	US-09-449-437A-16	Sequence 16, Appl1
572	10.4	45.2	50	3	US-08-482-369A-5	Sequence 5, Appl1	c 645	10.2	44.3	30	2	US-08-845-161A-44	Sequence 44, Appl1
573	10.4	45.2	50	3	US-08-482-369A-7	Sequence 7, Appl1	c 646	10.2	44.3	30	2	US-08-860-882A-1	Sequence 1, Appl1
574	10.4	45.2	50	3	US-08-482-369A-12	Sequence 12, Appl1	c 647	10.2	44.3	30	2	US-08-860-882A-3	Sequence 3, Appl1
575	10.4	45.2	50	3	US-08-482-369A-16	Sequence 16, Appl1	648	10.2	44.3	30	2	US-08-808-277A-42	Sequence 42, Appl1
576	10.4	45.2	50	3	US-09-009-217-18	Sequence 18, Appl1	649	10.2	44.3	30	3	US-08-746-160-49	Sequence 49, Appl1
577	10.4	45.2	50	3	US-09-009-217-22	Sequence 22, Appl1	650	10.2	44.3	30	3	US-08-810-324-44	Sequence 44, Appl1
578	10.4	45.2	50	3	US-09-009-656-18	Sequence 18, Appl1	c 651	10.2	44.3	30	4	US-09-370-751-44	Sequence 44, Appl1
579	10.4	45.2	50	3	US-09-009-656-22	Sequence 22, Appl1	c 652	10.2	44.3	30	4	US-08-748-547-17	Sequence 17, Appl1
580	10.4	45.2	50	5	PCT-US93-12388-112	Sequence 112, App	c 653	10.2	44.3	30	4	US-08-647-924-27	Sequence 27, Appl1
581	10.4	45.2	50	5	PCT-US93-12388-138	Sequence 138, App	654	10.2	44.3	30	5	PCT-US94-10957-25	Sequence 25, Appl1
582	10.4	45.2	50	5	PCT-US95-07439-5	Sequence 5, Appl1	655	10.2	44.3	31	1	US-08-350-884-46	Sequence 46, Appl1
583	10.4	45.2	50	5	PCT-US95-07439-7	Sequence 7, Appl1	656	10.2	44.3	31	1	US-08-440-548-46	Sequence 46, Appl1
584	10.4	45.2	50	5	PCT-US95-07439-12	Sequence 12, Appl1	657	10.2	44.3	31	1	US-08-709-173-46	Sequence 46, Appl1
585	10.4	45.2	50	5	PCT-US95-07439-16	Sequence 16, Appl1	c 658	10.2	44.3	31	1	US-08-469-421-15	Sequence 15, Appl1
586	10.2	44.3	16	3	US-08-181-664-35	Sequence 35, Appl1	c 659	10.2	44.3	31	1	US-08-250-975-15	Sequence 15, Appl1
587	10.2	44.3	18	1	US-08-686-336-2	Sequence 2, Appl1	c 660	10.2	44.3	31	2	US-08-605-002A-15	Sequence 15, Appl1
588	10.2	44.3	20	1	US-07-940-242A-81	Sequence 81, Appl1	661	10.2	44.3	31	2	US-08-709-177-46	Sequence 46, Appl1
589	10.2	44.3	20	1	US-08-384-490-7	Sequence 7, Appl1	c 662	10.2	44.3	31	2	US-08-950-449A-15	Sequence 15, Appl1
590	10.2	44.3	20	2	US-08-459-383-7	Sequence 7, Appl1	c 663	10.2	44.3	31	2	US-08-845-161A-12	Sequence 12, Appl1
591	10.2	44.3	20	2	US-08-466-337A-9	Sequence 9, Appl1	664	10.2	44.3	31	3	US-08-444-818-194	Sequence 194, App
592	10.2	44.3	20	2	US-08-757-653-164	Sequence 164, App	c 665	10.2	44.3	31	4	US-09-270-751-12	Sequence 12, Appl1
593	10.2	44.3	20	2	US-08-475-359-9	Sequence 9, Appl1	c 666	10.2	44.3	31	4	US-08-467-504-8	Sequence 8, Appl1
594	10.2	44.3	20	2	US-08-412-376-11	Sequence 11, Appl1	c 667	10.2	44.3	31	5	PCT-US94-10529-15	Sequence 15, Appl1
595	10.2	44.3	20	2	US-08-823-516-62	Sequence 62, Appl1	c 668	10.2	44.3	32	1	US-08-330-535A-17	Sequence 17, Appl1
596	10.2	44.3	20	3	US-08-465-887A-9	Sequence 9, Appl1	c 669	10.2	44.3	32	1	US-08-688-145-12	Sequence 12, Appl1
597	10.2	44.3	20	3	US-08-776-900C-4	Sequence 4, Appl1	c 670	10.2	44.3	32	2	US-08-838-844-17	Sequence 17, Appl1
598	10.2	44.3	20	3	US-08-759-038-103	Sequence 103, App	671	10.2	44.3	32	4	US-09-647-314-19	Sequence 19, Appl1
599	10.2	44.3	20	3	US-08-758-314-103	Sequence 103, App	c 672	10.2	44.3	32	5	PCT-US95-11985A-26	Sequence 26, Appl1
600	10.2	44.3	20	3	US-09-286-904-69	Sequence 69, Appl1	c 673	10.2	44.3	33	1	US-08-053-131-117	Sequence 117, App
601	10.2	44.3	20	4	US-09-268-195C-4	Sequence 4, Appl1	c 674	10.2	44.3	33	1	US-08-645-641-117	Sequence 117, App
602	10.2	44.3	20	4	US-09-488-671-36	Sequence 36, Appl1	c 675	10.2	44.3	33	1	US-07-853-408B-117	Sequence 117, App
603	10.2	44.3	20	4	US-09-313-932-272	Sequence 272, App	c 676	10.2	44.3	33	1	US-08-096-762-117	Sequence 117, App
604	10.2	44.3	21	1	US-08-317-432A-15	Sequence 15, Appl1	677	10.2	44.3	33	2	US-08-353-476-17	Sequence 17, Appl1
605	10.2	44.3	21	3	US-08-258-287B-80	Sequence 80, Appl1	c 678	10.2	44.3	33	2	US-08-308-865-117	Sequence 117, App
606	10.2	44.3	21	3	US-08-258-287B-81	Sequence 81, Appl1	c 679	10.2	44.3	33	2	US-08-596-319-20	Sequence 20, Appl1
607	10.2	44.3	21	3	US-08-368-704C-78	Sequence 78, Appl1	c 680	10.2	44.3	33	4	US-09-252-292-6	Sequence 6, Appl1
608	10.2	44.3	21	3	US-08-368-704C-79	Sequence 79, Appl1	c 681	10.2	44.3	33	4	US-09-042-353-309	Sequence 309, App
609	10.2	44.3	21	6	546668-40	Patent No. 546668	c 682	10.2	44.3	33	4	US-09-391-001-3	Sequence 3, Appl1
610	10.2	44.3	24	1	US-08-222-616-37	Sequence 37, Appl1	c 683	10.2	44.3	33	4	US-09-461-697-102	Sequence 102, App
611	10.2	44.3	24	2	US-08-859-998-695	Sequence 695, App	c 684	10.2	44.3	33	4	US-08-758-417A-157	Sequence 157, App

685	10.2	44.3	33	4	US-09-232-278A-6	Sequence 6, Appli	758	10.2	44.3	48	2	US-08-859-649-10	Sequence 10, Appl
c 686	10.2	44.3	33	5	PCT-US92-10983-117	Sequence 117, App	759	10.2	44.3	48	4	US-08-207-861-10	Sequence 10, Appl
c 687	10.2	44.3	34	1	US-08-230-002-3	Sequence 3, Appli	c 760	10.2	44.3	48	5	PCT-US96-03940-24	Sequence 24, Appl
688	10.2	44.3	34	2	US-08-417-330A-8	Sequence 8, Appli	c 761	10.2	44.3	49	1	US-08-608-617-2	Sequence 2, Appli
c 689	10.2	44.3	34	1	US-08-678-854-3	Sequence 3, Appli	c 762	10.2	44.3	49	2	US-08-652-558-20	Sequence 20, Appl
c 690	10.2	44.3	34	4	US-09-063-667-6	Sequence 6, Appli	c 763	10.2	44.3	49	2	US-08-931-830-2	Sequence 2, Appli
c 691	10.2	44.3	34	4	US-09-063-667-7	Sequence 7, Appli	c 764	10.2	44.3	49	2	US-08-989-394-16	Sequence 16, Appl
c 692	10.2	44.3	35	4	US-08-812-946A-6	Sequence 6, Appli	c 765	10.2	44.3	49	2	US-08-989-394-22	Sequence 22, Appl
c 693	10.2	44.3	36	1	US-08-451-240-43	Sequence 43, Appl	c 766	10.2	44.3	49	4	US-09-271-365-16	Sequence 16, Appl
694	10.2	44.3	36	1	US-08-723-896-31	Sequence 31, Appl	c 767	10.2	44.3	49	4	US-09-271-365-22	Sequence 22, Appl
c 695	10.2	44.3	36	2	US-08-470-846A-39	Sequence 39, Appl	c 768	10.2	44.3	49	4	US-09-384-195-2	Sequence 2, Appli
c 696	10.2	44.3	36	4	US-09-440-001-1	Sequence 1, Appli	c 769	10.2	44.3	50	1	US-08-171-389-364	Sequence 364, App
c 697	10.2	44.3	36	4	US-08-858-111-13	Sequence 13, Appl	c 770	10.2	44.3	50	1	US-08-123-936-364	Sequence 364, App
c 698	10.2	44.3	36	5	PCT-US94-12591-43	Sequence 43, Appl	c 771	10.2	44.3	50	1	US-08-472-194A-21	Sequence 21, Appl
c 699	10.2	44.3	37	1	US-08-217-327-15	Sequence 15, Appl	c 772	10.2	44.3	50	2	US-08-475-228A-364	Sequence 364, App
700	10.2	44.3	37	1	US-08-330-535A-27	Sequence 27, Appl	c 773	10.2	44.3	50	2	US-08-479-733A-5	Sequence 5, Appli
701	10.2	44.3	37	1	US-08-688-145-2	Sequence 2, Appli	c 774	10.2	44.3	50	2	US-08-479-733A-7	Sequence 7, Appli
702	10.2	44.3	37	2	US-08-838-844-27	Sequence 27, Appl	c 775	10.2	44.3	50	2	US-08-479-733A-12	Sequence 12, Appl
c 703	10.2	44.3	37	4	US-09-333-762B-10	Sequence 10, Appl	c 776	10.2	44.3	50	2	US-08-479-733A-16	Sequence 16, Appl
704	10.2	44.3	38	1	US-08-441-534A-2	Sequence 2, Appli	c 777	10.2	44.3	50	2	US-08-989-394-12	Sequence 12, Appl
705	10.2	44.3	38	1	US-08-616-398-8	Sequence 8, Appli	c 778	10.2	44.3	50	3	US-08-487-427-5	Sequence 5, Appli
706	10.2	44.3	38	1	US-08-629-752-2	Sequence 2, Appli	c 779	10.2	44.3	50	3	US-08-487-427-7	Sequence 7, Appli
707	10.2	44.3	38	1	US-08-682-218-25	Sequence 25, Appl	c 780	10.2	44.3	50	3	US-08-487-427-12	Sequence 12, Appl
708	10.2	44.3	38	1	US-08-802-991-2	Sequence 2, Appli	c 781	10.2	44.3	50	3	US-08-487-427-16	Sequence 16, Appl
709	10.2	44.3	38	2	US-08-963-946-22	Sequence 22, Appl	c 782	10.2	44.3	50	3	US-08-482-080A-364	Sequence 364, App
710	10.2	44.3	38	5	PCT-US95-07554-2	Sequence 2, Appli	c 783	10.2	44.3	50	3	US-08-479-727A-5	Sequence 5, Appli
711	10.2	44.3	39	2	US-08-561-521-24	Sequence 24, Appl	c 784	10.2	44.3	50	3	US-08-479-727A-7	Sequence 7, Appli
712	10.2	44.3	39	2	US-08-938-858-11	Sequence 11, Appl	c 785	10.2	44.3	50	3	US-08-479-727A-12	Sequence 12, Appl
713	10.2	44.3	39	3	US-09-289-751-2	Sequence 2, Appli	c 786	10.2	44.3	50	3	US-08-479-727A-16	Sequence 16, Appl
714	10.2	44.3	39	5	PCT-US95-01219-24	Sequence 24, Appl	c 787	10.2	44.3	50	3	US-08-482-369A-5	Sequence 5, Appli
715	10.2	44.3	40	1	US-08-199-507B-34	Sequence 34, Appl	c 788	10.2	44.3	50	3	US-08-482-369A-7	Sequence 7, Appli
716	10.2	44.3	40	1	US-08-441-828-34	Sequence 34, Appl	c 789	10.2	44.3	50	3	US-08-482-369A-12	Sequence 12, Appl
717	10.2	44.3	40	3	US-08-938-858-9	Sequence 9, Appli	c 790	10.2	44.3	50	3	US-08-482-369A-16	Sequence 16, Appl
718	10.2	44.3	40	3	US-09-289-751-1	Sequence 1, Appli	c 791	10.2	44.3	50	3	US-09-262-142-21	Sequence 21, Appl
719	10.2	44.3	40	4	US-09-091-725-6	Sequence 6, Appli	c 792	10.2	44.3	50	3	US-09-009-217-17-22	Sequence 18, Appl
720	10.2	44.3	41	1	US-08-531-747-2	Sequence 2, Appli	c 793	10.2	44.3	50	3	US-09-009-217-22	Sequence 22, Appl
721	10.2	44.3	41	1	US-08-531-749-2	Sequence 2, Appli	c 794	10.2	44.3	50	3	US-09-009-656-18	Sequence 18, Appl
722	10.2	44.3	41	1	US-08-781-432-2	Sequence 2, Appli	c 795	10.2	44.3	50	3	US-09-009-656-22	Sequence 22, Appl
c 723	10.2	44.3	41	2	US-08-561-521-25	Sequence 25, Appl	c 796	10.2	44.3	50	4	US-09-271-365-12	Sequence 12, Appl
724	10.2	44.3	41	2	US-08-854-041-2	Sequence 2, Appli	c 797	10.2	44.3	50	4	US-08-563-524A-13	Sequence 13, Appl
725	10.2	44.3	41	3	US-08-964-020-4	Sequence 4, Appli	c 798	10.2	44.3	50	4	US-08-563-524A-14	Sequence 14, Appl
c 726	10.2	44.3	41	5	PCT-US95-01219-25	Sequence 25, Appl	c 799	10.2	44.3	50	4	US-08-563-524A-15	Sequence 15, Appl
c 727	10.2	44.3	42	2	US-08-989-394-17	Sequence 17, Appl	c 800	10.2	44.3	50	4	US-08-563-524A-17	Sequence 17, Appl
c 728	10.2	44.3	42	4	US-09-271-365-17	Sequence 17, Appl	c 801	10.2	44.3	50	4	US-08-563-524A-18	Sequence 18, Appl
c 729	10.2	44.3	42	4	US-08-989-394-13	Sequence 13, Appl	c 802	10.2	44.3	50	4	US-08-563-524A-19	Sequence 19, Appl
730	10.2	44.3	43	4	US-09-289-380-1	Sequence 1, Appli	c 803	10.2	44.3	50	4	US-08-849-567A-21	Sequence 21, Appl
c 731	10.2	44.3	43	4	US-09-271-365-13	Sequence 13, Appl	c 804	10.2	44.3	50	4	US-09-298-886-19	Sequence 19, Appl
c 732	10.2	44.3	43	4	US-08-542-634-29	Sequence 29, Appl	c 805	10.2	44.3	50	4	US-09-298-886-25	Sequence 25, Appl
c 733	10.2	44.3	43	4	US-09-303-064-1	Sequence 1, Appli	c 806	10.2	44.3	50	4	US-09-298-886-28	Sequence 28, Appl
c 734	10.2	44.3	43	4	US-09-086-503-1	Sequence 1, Appli	c 807	10.2	44.3	50	5	PCT-US93-12388-364	Sequence 364, App
c 735	10.2	44.3	43	5	PCT-US95-13703-29	Sequence 29, Appl	c 808	10.2	44.3	50	5	PCT-US95-07439-5	Sequence 5, Appli
736	10.2	44.3	44	2	US-08-488-402A-117	Sequence 117, App	c 809	10.2	44.3	50	5	PCT-US95-07439-7	Sequence 7, Appli
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738	10.2	44.3	44	3	US-08-479-733A-18	Sequence 18, Appl	c 811	10.2	44.3	50	5	PCT-US95-07439-16	Sequence 16, Appl
739	10.2	44.3	44	3	US-08-487-427-18	Sequence 18, Appl	c 812	10.2	44.3	50	5	US-08-622-353-3	Sequence 3, Appli
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742	10.2	44.3	44	3	US-09-009-217-24	Sequence 24, Appl	c 815	10.2	44.3	50	5	US-08-353-700-4	Sequence 4, Appli
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745	10.2	44.3	45	5	PCT-US96-09472-117	Sequence 117, App	c 818	10.2	44.3	50	5	US-08-343-785-31	Sequence 31, Appl
c 746	10.2	44.3	45	1	US-07-885-689A-5	Sequence 5, Appli	c 819	10.2	44.3	50	5	US-08-343-785-33	Sequence 33, Appl
747	10.2	44.3	45	1	US-08-217-327-16	Sequence 16, Appl	c 820	10.2	44.3	50	5	US-08-048-975-6	Sequence 6, Appli
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c 753	10.2	44.3	46	1	US-08-608-617-4	Sequence 4, Appli	c 826	10.2	44.3	50	5	US-08-888-497-20	Sequence 20, Appl
c 754	10.2	44.3	46	2	US-08-931-830-4	Sequence 4, Appli	c 827	10.2	44.3	50	5	US-08-987-418A-5	Sequence 5, Appli
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c 756	10.2	44.3	46	4	US-08-990-823-108	Sequence 108, App	c 829	10.2	44.3	50	5	US-08-946-458-33	Sequence 33, Appl
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c 831	10	43.5	20	4	US-09-101-886B-92	Sequence 92, Appl	904	10	43.5	28	1	US-08-045-806-18	Sequence 18, Appl
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c 833	10	43.5	20	4	US-09-191-136-10	Sequence 10, Appl	c 906	10	43.5	28	1	US-07-920-281C-20	Sequence 20, Appl
c 834	10	43.5	20	4	US-09-191-136-24	Sequence 24, Appl	c 907	10	43.5	28	3	US-08-968-768B-7	Sequence 7, Appl
c 835	10	43.5	20	4	US-09-343-062-5	Sequence 5, Appl	c 908	10	43.5	28	3	US-08-905-359A-13	Sequence 13, Appl
c 836	10	43.5	20	4	US-09-489-869-72	Sequence 72, Appl	c 909	10	43.5	28	4	US-09-353-556-13	Sequence 13, Appl
c 837	10	43.5	20	4	US-09-489-869-73	Sequence 73, Appl	c 910	10	43.5	28	4	US-08-466-277-20	Sequence 20, Appl
c 838	10	43.5	20	4	US-09-344-491A-7	Sequence 7, Appl	c 911	10	43.5	29	6	5202236-10	Patent No. 5202236
c 839	10	43.5	20	4	US-09-183-959-15	Sequence 15, Appl	c 912	10	43.5	30	2	US-08-713-939A-66	Sequence 66, Appl
c 840	10	43.5	20	4	US-09-412-484-5	Sequence 5, Appl	c 913	10	43.5	30	2	US-08-460-529B-4	Sequence 4, Appl
c 841	10	43.5	20	4	US-09-362-230-20	Sequence 20, Appl	c 914	10	43.5	30	3	US-08-874-563-14	Sequence 14, Appl
c 842	10	43.5	20	4	US-09-624-693A-5	Sequence 5, Appl	c 915	10	43.5	30	4	US-09-091-590A-18	Sequence 18, Appl
c 843	10	43.5	20	4	US-09-354-243B-21	Sequence 21, Appl	c 916	10	43.5	30	4	US-09-036-579-66	Sequence 66, Appl
c 844	10	43.5	20	5	PCF-US94-07926-20	Sequence 20, Appl	c 917	10	43.5	30	4	US-09-485-636-5	Sequence 5, Appl
c 845	10	43.5	21	1	US-08-214-636-1	Sequence 1, Appl	c 918	10	43.5	31	1	US-08-019-870-25	Sequence 25, Appl
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c 847	10	43.5	21	1	US-08-434-411-31	Sequence 31, Appl	c 920	10	43.5	33	1	US-08-019-870-26	Sequence 26, Appl
c 848	10	43.5	21	1	US-08-434-411-35	Sequence 35, Appl	c 921	10	43.5	33	1	US-08-741-881-63	Sequence 63, Appl
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c 850	10	43.5	21	1	US-08-434-402-31	Sequence 31, Appl	c 923	10	43.5	33	2	US-08-739-167-63	Sequence 63, Appl
c 851	10	43.5	21	1	US-08-434-402-35	Sequence 35, Appl	c 924	10	43.5	33	3	US-08-404-796-63	Sequence 63, Appl
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c 854	10	43.5	21	1	US-08-783-288-35	Sequence 35, Appl	c 927	10	43.5	33	3	US-08-776-511-5	Sequence 5, Appl
c 855	10	43.5	21	2	US-08-687-916-8	Sequence 8, Appl	c 928	10	43.5	33	4	US-09-350-399-63	Sequence 63, Appl
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c 859	10	43.5	21	2	US-08-890-640-35	Sequence 35, Appl	c 932	10	43.5	34	2	US-08-537-811-10	Sequence 10, Appl
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c 861	10	43.5	21	4	US-09-521-154-5	Sequence 5, Appl	c 934	10	43.5	34	3	US-08-961-083-315	Sequence 315, App
c 862	10	43.5	21	4	US-09-091-590A-19	Sequence 19, Appl	c 935	10	43.5	35	3	US-09-164-023-1	Sequence 1, Appl
c 863	10	43.5	21	4	US-09-138-614-8	Sequence 8, Appl	c 936	10	43.5	35	4	US-08-869-276-3	Sequence 3, Appl
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c 867	10	43.5	21	6	5194592-58	Patent No. 5194592	c 940	10	43.5	36	1	US-08-324-301-25	Sequence 25, Appl
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c 875	10	43.5	22	4	US-09-130-079-19	Sequence 19, Appl	c 948	10	43.5	37	1	US-08-199-779-4	Sequence 4, Appl
c 876	10	43.5	22	4	US-09-130-079-20	Sequence 20, Appl	c 949	10	43.5	37	1	US-08-579-667-12	Sequence 12, Appl
c 877	10	43.5	22	4	US-09-130-079-21	Sequence 21, Appl	c 950	10	43.5	37	2	US-08-472-659-12	Sequence 12, Appl
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c 879	10	43.5	22	5	PCF-US92-02854-6	Sequence 6, Appl	c 952	10	43.5	37	2	US-08-448-561-24	Sequence 24, Appl
c 880	10	43.5	22	5	PCF-US95-08604-75	Sequence 75, Appl	c 953	10	43.5	37	2	US-08-611-977-12	Sequence 12, Appl
c 881	10	43.5	23	2	US-08-808-620-2	Sequence 2, Appl	c 954	10	43.5	37	3	US-08-578-615A-107	Sequence 107, App
c 882	10	43.5	24	1	US-08-578-709-17	Sequence 17, Appl	c 955	10	43.5	37	3	US-08-987-418A-3	Sequence 3, Appl
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c 884	10	43.5	25	1	US-08-155-746-6	Sequence 6, Appl	c 957	10	43.5	37	4	US-09-191-136-9	Sequence 9, Appl
c 885	10	43.5	25	1	US-08-341-148-1	Sequence 1, Appl	c 958	10	43.5	37	4	US-09-343-062-3	Sequence 3, Appl
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c 887	10	43.5	25	1	US-08-341-148-24	Sequence 24, Appl	c 960	10	43.5	37	5	PCF-US94-07770-107	Sequence 107, App
c 888	10	43.5	25	1	US-08-264-861A-8	Sequence 8, Appl	c 961	10	43.5	38	2	US-08-942-423-66	Sequence 66, Appl
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c 893	10	43.5	25	4	US-08-776-844-8	Sequence 8, Appl	c 966	10	43.5	40	1	US-08-199-507B-16	Sequence 16, Appl
c 894	10	43.5	25	5	PCF-US94-00771-6	Sequence 6, Appl	c 967	10	43.5	40	1	US-08-199-507B-30	Sequence 30, Appl
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c 897	10	43.5	25	5	PCF-US94-14096-24	Sequence 24, Appl	c 970	10	43.5	40	4	US-09-371-257A-1	Sequence 1, Appl
c 898	10	43.5	25	5	PCF-US95-07784-8	Sequence 8, Appl	c 971	10	43.5	40	4	US-09-052-521C-17	Sequence 17, Appl
c 899	10	43.5	26	3	US-09-009-156-10	Sequence 10, Appl	c 972	10	43.5	42	1	US-08-530-492-46	Sequence 46, Appl
c 900	10	43.5	26	4	US-09-372-154-10	Sequence 10, Appl	c 973	10	43.5	42	4	US-08-906-517-46	Sequence 46, Appl
c 901	10	43.5	27	2	US-08-636-597-6	Sequence 6, Appl	c 974	10	43.5	42	4	US-09-130-079-2	Sequence 2, Appl
c 902	10	43.5	27	3	US-08-777-708C-11	Sequence 11, Appl	c 975	10	43.5	42	4	US-09-130-079-5	Sequence 5, Appl
c 903	10	43.5	27	4	US-09-253-396A-180	Sequence 180, App	c 976	10	43.5	42	4	US-09-130-079-6	Sequence 6, Appl

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c 980 10 43.5 43 1 US-08-214-636-9 Sequence 9, Appl
c 981 10 43.5 43 4 US-08-821-994-1 Sequence 1, Appl
c 982 10 43.5 45 5 PCT-US96-09430-1 Sequence 1, Appl
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c 984 10 43.5 46 1 US-08-530-492-40 Sequence 40, Appl
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c 988 10 43.5 47 1 US-07-990-893-3 Sequence 3, Appl
c 989 10 43.5 48 1 US-08-295-670-4 Sequence 4, Appl
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c 996 10 43.5 48 5 PCT-US94-09851-36 Sequence 36, Appl
c 997 10 43.5 50 1 US-08-171-389-513 Sequence 513, App
c 998 10 43.5 50 1 US-08-207-901-29 Sequence 29, Appl
c 999 10 43.5 50 1 US-08-123-936-513 Sequence 513, App
1000 10 43.5 50 2 US-08-475-228A-513 Sequence 513, App

ALIGNMENTS

RESULT 1
US-08-624-545-66
; Sequence 66, Application US/08624545
; Patent No. 5817495
; GENERAL INFORMATION:
; APPLICANT: Pedersen, Anders
; APPLICANT: Vind, Jesper
; APPLICANT: Svendsen, Allan
; APPLICANT: Cherry, Joel
; APPLICANT: Lamsa, Michael
; APPLICANT: Schneider, Palte
; APPLICANT: Jensen, Birger
; TITLE OF INVENTION: H202-Stable Peroxidase Variants
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: No. 5817495o No. 5817495disk of No. 5817495th America
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/624,545
; FILING DATE: 07-MAY-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Agris, Cheryl H.
; REGISTRATION NUMBER: 34,086
; REFERENCE/DOCKET NUMBER: 4072.204
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 867-0123
; TELEFAX: (212) 878-9655
; INFORMATION FOR SEQ ID NO: 66:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
* US-08-624-545-66

Query Match 63.5%; Score 14.6; DB 1; Length 23;
Best Local Similarity 81.0%; Pred. No. 2.2e+02;
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 accaggcgctctcgtgggccac 21
| ||||| ||||| |||||
Db 3 AACAGGGCGCTCGTTGGACAC 23

RESULT 2
US-09-242-690A-20/c
; Sequence 20, Application US/09242690A
; Patent No. 6284534
; GENERAL INFORMATION:
; APPLICANT: KONDO, KEIJI
; APPLICANT: MURA, YUTAKA
; TITLE OF INVENTION: YEAST VECTOR AND METHOD OF PRODUCING PROTEINS USING THE
; TITLE OF INVENTION: SAME
; FILE REFERENCE: 049441/0118
; CURRENT APPLICATION NUMBER: US/09/242,690A
; CURRENT FILING DATE: 1999-02-23
; PRIOR APPLICATION NUMBER: PCT/JP97/02924
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: JP 8/241062
; PRIOR FILING DATE: 1996-08-23
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-242-690A-20

Query Match 61.7%; Score 14.2; DB 4; Length 30;
Best Local Similarity 84.2%; Pred. No. 3.3e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 25 ACCAGGCGTTTGGCGGGGCC 7

RESULT 3
US-08-075-193-16/c
; Sequence 16, Application US/08075193
; Patent No. 5547868
; GENERAL INFORMATION:
; APPLICANT: MILLER, WALTER L.
; APPLICANT: HARIKRISHNA, JENNIFER A.
; APPLICANT: BLACK, STEPHEN M.
; TITLE OF INVENTION: CHOLESTEROL DISPOSAL FUSION ENZYMES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: COOLEY GODWARD CASTRO HUDDLESON & TATUM
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; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/075,193
; FILING DATE: 09-JUN-1993
; CLASSIFICATION: 435

; STREET: P.O. Box 828
; CITY: Bloomfield Hills
; STATE: Michigan
; COUNTRY: USA
; ZIP: 48303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/306,546C
; FILING DATE: September 15, 1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, DeAnn F.
; REGISTRATION NUMBER: 36,683
; REFERENCE/DOCKET NUMBER: 6550-00003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (810)641-1600
; TELEFAX: (810)641-0270
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; TOPOLOGY: linear
; MOLECULE TYPE: primer
; US-08-306-546C-4

Query Match 59.1%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 6.2e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 aggcgtctcgtggccacat 23
||| ||||| |||||
Db 20 AGGTGTCGTAGCCACTT 1

RESULT 7
US-08-530-524A-4/C
; Sequence 4, Application US/08530524A
; Patent No. 5837836
; GENERAL INFORMATION:
; APPLICANT: Friderici, Karen
; APPLICANT: Jones, Margaret
; APPLICANT: Chen, Hong
; APPLICANT: Cavanagh, Kevin
; TITLE OF INVENTION: Bovine Beta-Mannosidase Gene and Methods
; TITLE OF INVENTION: of Use
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Harness, Dickey & Pierce, P.L.C.
; STREET: P.O. Box 828
; CITY: Bloomfield Hills
; STATE: Michigan
; COUNTRY: USA
; ZIP: 48303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/530,524A
; FILING DATE: September 19, 1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, DeAnn F.
; REGISTRATION NUMBER: 36,683
; REFERENCE/DOCKET NUMBER: 6550-00003DVA
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (810)641-1600
; TELEFAX: (810)641-0270
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: primer
; US-08-530-524A-4

Query Match 59.1%; Score 13.6; DB 2; Length 20;
Best Local Similarity 80.0%; Pred. No. 6.2e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 aggcgtctcgtggccacat 23
||| ||||| |||||
Db 20 AGGTGTCGTAGCCACTT 1

RESULT 8
US-07-946-421-36
; Sequence 36, Application US/07946421
; Patent No. 5558864
; GENERAL INFORMATION:
; APPLICANT: Bendig, Mary M.
; APPLICANT: Kettleborough, Catherine A.
; APPLICANT: Saldanha, Jose
; TITLE OF INVENTION: Humanized and Chimeric Monoclonal
; TITLE OF INVENTION: Antibodies
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Millen, White, Zelano & Branigan, P.C.
; STREET: 2200 Clarendon Boulevard, Suite 1400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22201

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/946,421
; FILING DATE: 06-NOV-1992
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/EP92/00480
; FILING DATE: 04-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 911933892
; FILING DATE: 06-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hamlet-King, Diana
; REGISTRATION NUMBER: 33,302
; REFERENCE/DOCKET NUMBER: Merck 1430
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-243-6333
; TELEFAX: 703-243-6410
; TELEX: 64191
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 45 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-07-946-421-36

Query Match 59.1%; Score 13.6; DB 1; Length 45;
Best Local Similarity 80.0%; Pred. No. 6.4e+02;

Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 accaggcgtctcgtggcca 20
||| ||| ||| ||| ||| |||
Db 23 ACCTGGCTTCTGCTGGCCA 42

RESULT 9

US-08-459-310-6/c
; Sequence 6, Application US/08459310
; Patent No. 5645817
; GENERAL INFORMATION:
; APPLICANT: Seemann, Gerhard
; APPLICANT: Bosslet, Klaus
; TITLE OF INVENTION: Granulocyte-Binding Antibody Constructs,
; TITLE OF INVENTION: Their Preparation and Use
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,310
; FILING DATE:
; CLASSIFICATION: 424

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/100,963
; FILING DATE: 03-AUG-1993
; APPLICATION NUMBER: DE P 422 58 53.7
; FILING DATE: 05-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Wadler, Linda A.
; REGISTRATION NUMBER: 33,218
; REFERENCE/DOCKET NUMBER: 02481.1317-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400

INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 45 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-459-310-6

Query Match 59.1%; Score 13.6; DB 1; Length 45;
Best Local Similarity 80.0%; Pred. No. 6.4e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 accaggcgtctcgtggcca 20
||| ||| ||| ||| ||| |||
Db 23 ACCTGGCTTCTGCTGGCCA 4

RESULT 10

US-08-116-778E-33
; Sequence 33, Application US/08116778E
; Patent No. 5830470
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, KAZUYASU
; APPLICANT: KOIKE, MASAMICHI
; APPLICANT: SHITARA, KENYA

; APPLICANT: HANAI, NOBUO
; APPLICANT: KUWANA, YOSHIHISA
; APPLICANT: HASEGAWA, MAMORU
; TITLE OF INVENTION: HUMANIZED ANTIBODIES
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/116,778E
; FILING DATE: 07-SEP-93
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARY J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 249-59
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)816-4000
; TELEFAX: (703)816-4100
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 45 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid, synthetic DNA
US-08-116-778E-33

Query Match 59.1%; Score 13.6; DB 2; Length 45;
Best Local Similarity 80.0%; Pred. No. 6.4e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 accaggcgtctcgtggcca 20
||| ||| ||| ||| ||| |||
Db 25 ACCTGGCTTCTGCTGGCCA 44

RESULT 11

US-08-438-562-33
; Sequence 33, Application US/08438562
; Patent No. 5874255
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, KAZUYASU
; APPLICANT: KOIKE, MASAMICHI
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: KUWANA, YOSHIHISA
; APPLICANT: HASEGAWA, MAMORU
; TITLE OF INVENTION: HUMANIZED ANTIBODIES
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/438,562
FILING DATE: 10-MAY-95
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/116,778
FILING DATE: 07-SEP-93
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 249-76
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)816-4000
TELEFAX: (703)816-4100
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid, synthetic DNA
US-08-438-562-33

Query Match 59.1%; Score 13.6; DB 2; Length 45;
Best Local Similarity 80.0%; Pred. No. 6.4e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 accaggcgtctcgtgggcca 20
||| ||| ||| ||| ||| |||
Db 25 ACCTGGCTTCTGGTGTGCCA 44

RESULT 12
US-08-483-528B-33
Sequence 33, Application US/08483528B
Patent No. 5939532
GENERAL INFORMATION:
APPLICANT: NAKAMURA, KAZUYASU
APPLICANT: KOIKE, MASAMICHI
APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: KUWANA, YOSHITHISA
APPLICANT: HASEGAWA, MAMORU
TITLE OF INVENTION: HUMANIZED ANTIBODIES
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHVE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,528B
FILING DATE: 07-JUN-95
CLASSIFICATION: 536
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)816-4000
TELEFAX: (703)816-4100
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid, synthetic DNA
US-08-483-528B-33

Query Match 59.1%; Score 13.6; DB 2; Length 45;
Best Local Similarity 80.0%; Pred. No. 6.4e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 accaggcgtctcgtgggcca 20
||| ||| ||| ||| ||| |||
Db 25 ACCTGGCTTCTGGTGTGCCA 44

RESULT 13
US-08-673-799C-33
Sequence 33, Application US/08673799C
Patent No. 6042828
GENERAL INFORMATION:
APPLICANT: NAKAMURA, KAZUYASU
APPLICANT: KOIKE, MASAMICHI
APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: KUWANA, YOSHITHISA
APPLICANT: HASEGAWA, MAMORU
TITLE OF INVENTION: HUMANIZED ANTIBODIES
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHVE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/673,799C
FILING DATE: 27-JUN-96
CLASSIFICATION: 536
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)816-4000
TELEFAX: (703)816-4100
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid, synthetic DNA
US-08-673-799C-33

Query Match 59.1%; Score 13.6; DB 3; Length 45;
Best Local Similarity 80.0%; Pred. No. 6.4e+02;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 accaggcgtctcgtgggcca 20
||| ||| ||| ||| ||| |||
Db 25 ACCTGGCTTCTGGTGTGCCA 44

RESULT 14
US-08-779-764A-60/c
Sequence 60, Application US/08779764A
Patent No. 6057094
GENERAL INFORMATION:
APPLICANT: de la Torre, Juan C.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SCREENING
OF HUMAN BORNA DISEASE VIRUS
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: THE SCRIPPS RESEARCH INSTITUTE

STREET: 10550 No. 6057094th Torrey Pines Road, TPC-8
CITY: La Jolla
STATE: California
COUNTRY: United States
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/779,764A
FILING DATE: 16-DEC-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSRI 465.0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 784-2937
TELEFAX: (619) 784-9399
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-779-764A-60

Query Match 58.3%; Score 13.4; DB 3; Length 27;
Best Local Similarity 73.9%; Pred. No. 7.8e+02;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 accagggtctcgtgggccacat 23
| ||||| ||| |||
Db 23 ATCAGGCGTCTCCGGGTGGCAT 1

RESULT 15

US-08-930-274-5
Sequence 5, Application US/08930274
Patent No. 5932441
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
APPLICANT:
TITLE OF INVENTION: VECTORS FOR DIFFERENTIAL EXPRESSION
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
STREET: 2033 K Street, N.W., Suite 800
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/930,274
FILING DATE: September 29, 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95302196.1
FILING DATE: 31-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB 96/00765

FILING DATE: 29-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-8200
TELEFAX: 202-721-8250
TELEX:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "synthetic primer"
US-08-930-274-5

Query Match 58.3%; Score 13.4; DB 2; Length 42;
Best Local Similarity 73.9%; Pred. No. 7.9e+02;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 accagggtctcgtgggccacat 23
| ||||| ||| |||
Db 9 AGCATGCATCTAGAGGGCGGCAT 31

Search completed: August 17, 2002, 23:24:34
Job time: 4099 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 17, 2002, 21:27:35 ; Search time 1607.6 Seconds
(without alignments)
193.101 Million cell updates/sec

Title: US-09-700-906A-3
Perfect score: 23
Sequence: 1 accaggcgtctctgggccacat 23

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 89578

Minimum DB seq length: 0
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database :

- EST:*
- 1: em_estba:*
 - 2: em_esthum:*
 - 3: em_estin:*
 - 4: em_estmu:*
 - 5: em_estov:*
 - 6: em_estpl:*
 - 7: em_estro:*
 - 8: em_htc:*
 - 9: gb_est1:*
 - 10: gb_est2:*
 - 11: gb_htc:*
 - 12: gb_gss:*
 - 13: em_gss_hum:*
 - 14: em_gss_inv:*
 - 15: em_gss_pln:*
 - 16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	14.4	62.6	32	10	BG545479 602572715
2	14	60.9	50	9	AU106915 AU106915
3	13.6	59.1	34	9	AI097023 ozz2e03.x
C 4	13.2	57.4	34	9	AI537615 tp05d08.x
5	13.2	57.4	50	9	AU102952 AU102952
C 6	13.2	57.4	50	9	AU106296 AU106296
C 7	13	56.5	44	10	T64778 YC25h10.r1
8	12.6	54.8	32	10	BM395935 5009-0-14
9	12.6	54.8	43	9	AI685223 wc70e01.x
10	12.6	54.8	50	9	AU106914 AU106914
11	12.6	54.8	50	9	AU106917 AU106917
12	12.6	54.8	50	9	AU106918 AU106918
13	12.6	54.8	50	9	AU106920 AU106920
C 14	12.6	54.8	50	12	AZ789608 2M0037L01
15	12.4	53.9	38	12	AZ309417 1M0013G12
16	12.4	53.9	50	9	AU102221 AU102221
17	12.4	53.9	50	10	BE547372 601072933

c 91	10.8	47.0	25	12	AZ782142	AZ782142 2M0022H10	164	10.4	45.2	46	12	AZ445453
c 92	10.8	47.0	34	12	TA102C06P	AL462338 T. brucei	c 165	10.4	45.2	48	10	AA934014
c 93	10.8	47.0	37	9	AA149901	AA149901 zo02f05.r	166	10.4	45.2	48	10	BE622110
c 94	10.8	47.0	37	10	W05633	W05633 za90d08.r1	167	10.4	45.2	49	9	AA045123
c 95	10.8	47.0	40	9	AA933656	AA933656 om56d08.s	c 168	10.4	45.2	50	9	AU102253
c 96	10.8	47.0	43	9	AT679845	AT679845 tu66e07.x	c 169	10.4	45.2	50	9	AU102469
c 97	10.8	47.0	44	12	AZ441861	AZ441861 IM0234D18	c 170	10.4	45.2	50	9	AU102478
c 98	10.8	47.0	45	10	B1388653	B1388653 EST-CD34N	c 171	10.4	45.2	50	9	AU104209
c 99	10.8	47.0	46	10	Z19605	Z19605 HSA00AAH P	172	10.4	45.2	50	9	AU104425
c 100	10.8	47.0	48	9	AI313698	AI313698 EST010 Mo	173	10.4	45.2	50	9	AU105619
c 101	10.8	47.0	49	9	AA948716	AA948716 oq45h05.s	174	10.4	45.2	50	9	AU105922
c 102	10.8	47.0	49	9	AA975152	AA975152 om99c07.s	c 175	10.4	45.2	50	9	AU107936
c 103	10.8	47.0	50	9	AU102888	AU102888 AU102888	176	10.2	44.3	26	12	AZ436027
c 104	10.8	47.0	50	9	AU103357	AU103357 AU103357	177	10.2	44.3	29	12	TA71H09Q
c 105	10.8	47.0	50	9	AU103358	AU103358 AU103358	c 178	10.2	44.3	30	10	BE727670
c 106	10.8	47.0	50	9	AU103359	AU103359 AU103359	179	10.2	44.3	31	12	AZ432033
c 107	10.8	47.0	50	9	AU103361	AU103361 AU103361	180	10.2	44.3	32	12	AZ597602
c 108	10.8	47.0	50	9	AU104872	AU104872 AU104872	181	10.2	44.3	34	9	AA747497
c 109	10.8	47.0	50	9	AU104878	AU104878 AU104878	182	10.2	44.3	34	9	AA887400
c 110	10.8	47.0	50	9	AU104879	AU104879 AU104879	183	10.2	44.3	34	9	AI552428
c 111	10.8	47.0	50	9	AU104893	AU104893 AU104893	c 184	10.2	44.3	34	9	AA221932
c 112	10.8	47.0	50	9	AU104917	AU104917 AU104917	185	10.2	44.3	34	10	BF973182
c 113	10.8	47.0	50	9	AU105960	AU105960 AU105960	c 186	10.2	44.3	34	12	TA80A07Q
c 114	10.8	47.0	50	9	AU106905	AU106905 AU106905	c 187	10.2	44.3	35	12	AZ780177
c 115	10.6	46.1	25	9	AI608697	AI608697 tw26b02.x	c 188	10.2	44.3	38	10	BG390448
c 116	10.6	46.1	31	9	AA443732	AA443732 zw92d10.r	189	10.2	44.3	38	10	D19984
c 117	10.6	46.1	34	9	AI270065	AI270065 qt91f01.x	c 190	10.2	44.3	39	10	BJ063725
c 118	10.6	46.1	37	9	AA974682	AA974682 op29b04.s	c 191	10.2	44.3	40	9	AI123628
c 119	10.6	46.1	37	10	BG976503	BG976503 602846752	c 192	10.2	44.3	40	10	R77790
c 120	10.6	46.1	37	10	W05633	W05633 za90d08.r1	c 193	10.2	44.3	41	12	AZ776137
c 121	10.6	46.1	40	9	AA687193	AA687193 nu26e05.s	c 194	10.2	44.3	42	12	AZ759249
c 122	10.6	46.1	40	10	BF340179	BF340179 602036555	c 195	10.2	44.3	42	12	TA130G07P
c 123	10.6	46.1	40	12	AZ651473	AZ651473 IM0522N07	c 196	10.2	44.3	43	9	AA074398
c 124	10.6	46.1	43	9	AI2020738	AI2020738 ub01h04.r	c 197	10.2	44.3	43	9	AI588855
c 125	10.6	46.1	47	10	BI221669	BI221669 602937102	c 198	10.2	44.3	45	12	AZ309694
c 126	10.6	46.1	49	9	AI789860	AI789860 ue65d12.r	c 199	10.2	44.3	45	9	AA982418
c 127	10.6	46.1	50	9	AU103177	AU103177 AU103177	c 200	10.2	44.3	47	9	AW250812
c 128	10.6	46.1	50	9	AU104426	AU104426 AU104426	201	10.2	44.3	47	12	AZ615317
c 129	10.6	46.1	50	9	AU104427	AU104427 AU104427	c 202	10.2	44.3	47	12	TA100F09Q
c 130	10.6	46.1	50	9	AU104429	AU104429 AU104429	c 203	10.2	44.3	49	9	AI195300
c 131	10.6	46.1	50	9	AU104430	AU104430 AU104430	c 204	10.2	44.3	49	9	AI493938
c 132	10.6	46.1	50	9	AU104946	AU104946 AU104946	205	10.2	44.3	50	10	BF203474
c 133	10.6	46.1	50	9	AU104947	AU104947 AU104947	206	10.2	44.3	50	9	AI438119
c 134	10.6	46.1	50	9	AU104966	AU104966 AU104966	c 207	10.2	44.3	50	9	AU102728
c 135	10.6	46.1	50	9	AU104967	AU104967 AU104967	c 208	10.2	44.3	50	9	AU102729
c 136	10.6	46.1	50	9	AU106297	AU106297 AU106297	c 209	10.2	44.3	50	9	AU102730
c 137	10.6	46.1	50	9	AU106306	AU106306 AU106306	c 210	10.2	44.3	50	9	AU102732
c 138	10.6	46.1	50	9	AU107261	AU107261 AU107261	211	10.2	44.3	50	9	AU102860
c 139	10.6	46.1	50	9	AU107609	AU107609 AU107609	212	10.2	44.3	50	9	AU102972
c 140	10.6	46.1	50	9	AU107610	AU107610 AU107610	213	10.2	44.3	50	9	AU103388
c 141	10.6	46.1	50	9	AU107939	AU107939 AU107939	c 214	10.2	44.3	50	9	AU103970
c 142	10.6	46.1	50	9	AW248108	AW248108 2819599.s	215	10.2	44.3	50	9	AU106605
c 143	10.6	46.1	50	10	T62585	T62585 yc04a07.r1	216	10.2	44.3	50	9	AU107339
c 144	10.4	45.2	21	12	AZ758704	AZ758704 IM0550A20	217	10.2	44.3	50	9	AU107830
c 145	10.4	45.2	24	12	AZ936903	AZ936903 2M0193E20	218	10.2	44.3	50	9	AU107832
c 146	10.4	45.2	28	12	AQ254833	AQ254833 EP1212138	219	10.2	44.3	50	9	AU107833
c 147	10.4	45.2	31	10	BE367877	BE367877 601282104	c 220	10.2	44.3	50	12	AZ800436
c 148	10.4	45.2	34	9	AI3366127	AI3366127 ao94f04.x	221	10.2	44.3	50	12	AZ917998
c 149	10.4	45.2	34	9	AI589397	AI589397 tr61h11.x	222	10.2	44.3	50	12	BH624322
c 150	10.4	45.2	35	12	AZ654998	AZ654998 IM0529L12	c 223	10	43.5	23	12	TA338E01P
c 151	10.4	45.2	36	12	AZ828771	AZ828771 2M0106A02	224	10	43.5	25	10	BH399506
c 152	10.4	45.2	37	9	AI755616	AI755616 ETEStea38	c 225	10	43.5	26	12	AZ779432
c 153	10.4	45.2	37	12	BH129921	BH129921 G-6C8.f M	c 226	10	43.5	29	10	BM395762
c 154	10.4	45.2	38	10	BF144195	BF144195 601786804	227	10	43.5	31	9	AA755576
c 155	10.4	45.2	39	12	AZ491251	AZ491251 IM0324N11	228	10	43.5	31	9	AI651828
c 156	10.4	45.2	40	12	TA96H01Q	TA96H01Q T. brucei	c 229	10	43.5	33	12	AZ304883
c 157	10.4	45.2	43	9	AW247061	AW247061 2822604.s	230	10	43.5	33	12	AZ805302
c 158	10.4	45.2	43	10	BI462985	BI462985 603204504	c 231	10	43.5	34	10	BF579942
c 159	10.4	45.2	43	12	AZ514559	AZ514559 IM0361M10	232	10	43.5	34	12	AZ492829
c 160	10.4	45.2	43	12	AZ658528	AZ658528 IM0535C14	233	10	43.5	34	12	AZ628045
c 161	10.4	45.2	46	9	AA019274	AA019274 ze56h10.s	234	10	43.5	35	12	AZ621958
c 162	10.4	45.2	46	9	AA878878	AA878878 of88h03.s	235	10	43.5	36	10	BG718554
c 163	10.4	45.2	46	9	AI471447	AI471447 tml1f04.x	c 236	10	43.5	36	10	BG974649

c 237	10	43.5	36	10	BT109794	BT109794 6029001168	c 310	9.8	42.6	45	10	BM397811	BM397811 5009-0-37
c 238	10	43.5	37	9	AA048244	AA048244 mj27a04.r	311	9.8	42.6	46	9	AI744340	AI744340 tr09q03.x
c 239	10	43.5	37	9	AI683252	AI683252 tx02e12.x	312	9.8	42.6	46	9	AI917121	AI917121 ts052a12.x
c 240	10	43.5	37	10	N91581	N91581 zb24b07.s1	313	9.8	42.6	46	9	AA630952	AA630952 qg76a01.s
c 241	10	43.5	38	9	AV833714	AV833714 AV833714	c 314	9.8	42.6	46	10	BI651438	BI651438 603298178
c 242	10	43.5	39	10	BF036837	BF036837 601462043	c 315	9.8	42.6	46	12	AZ785255	AZ785255 2M0029106
c 243	10	43.5	40	10	H87341	H87341 yw16c03.s1	c 316	9.8	42.6	47	12	AZ784478	AZ784478 2M0027K02
c 244	10	43.5	41	10	BJ077957	BJ077957 BJ077957	c 317	9.8	42.6	48	10	BI834201	BI834201 603084104
c 245	10	43.5	41	10	BM399562	BM399562 5009-0-59	c 318	9.8	42.6	48	12	AZ576659	AZ576659 AST-TD1.4
c 246	10	43.5	41	12	AZ990630	AZ990630 2M0274M23	c 319	9.8	42.6	48	12	AZ694184	AZ694184 AST-TD1.4
c 247	10	43.5	42	10	BG912536	BG912536 602806638	c 320	9.8	42.6	49	10	D11784	D11784 HUMH01F06
c 248	10	43.5	42	10	BI656802	BI656802 603281484	c 321	9.8	42.6	50	9	AU102606	AU102606 AU102606
c 249	10	43.5	42	10	BF527907	BF527907 602041058	c 322	9.8	42.6	50	9	AU103951	AU103951 AU103951
c 250	10	43.5	43	9	AI367697	AI367697 qv75d12.x	323	9.8	42.6	50	9	AU105396	AU105396 AU105396
c 251	10	43.5	43	9	AI627640	AI627640 ty81a12.x	324	9.8	42.6	50	9	AU105399	AU105399 AU105399
c 252	10	43.5	43	9	W25159	W25159 zb69d02.r1	325	9.8	42.6	50	9	AU105400	AU105400 AU105400
c 253	10	43.5	43	12	AZ447897	AZ447897 1M0245G17	326	9.8	42.6	50	9	AU105402	AU105402 AU105402
c 254	10	43.5	44	10	R78925	R78925 y187c07.s1	c 327	9.8	42.6	50	9	AU105696	AU105696 AU105696
c 255	10	43.5	44	12	AQ0902830	AQ0902830 K16110-T7	c 328	9.8	42.6	50	9	AU105697	AU105697 AU105697
c 256	10	43.5	45	12	AZ484607	AZ484607 1M0311N10	329	9.8	42.6	50	9	AU105851	AU105851 AU105851
c 257	10	43.5	46	9	AA671439	AA671439 vn81h12.r	c 330	9.8	42.6	50	9	AU105858	AU105858 AU105858
c 258	10	43.5	46	9	AA537144	AA537144 vk45d06.r	c 331	9.8	42.6	50	9	AU105919	AU105919 AU105919
c 259	10	43.5	46	12	AZ810685	AZ810685 2M0076G24	332	9.8	42.6	50	9	AU106286	AU106286 AU106286
c 260	10	43.5	47	12	AZ957982	AZ957982 2M0225L02	c 333	9.8	42.6	50	9	AU106354	AU106354 AU106354
c 261	10	43.5	49	9	AA993146	AA993146 qt77a10.s	334	9.8	42.6	50	9	AU107117	AU107117 AU107117
c 262	10	43.5	49	9	AI192472	AI192472 qe65f04.x	335	9.8	42.6	50	9	AU107296	AU107296 AU107296
c 263	10	43.5	49	10	T91886	T91886 yd54f05.s1	336	9.8	42.6	50	9	AU107297	AU107297 AU107297
c 264	10	43.5	49	12	AZ613610	AZ613610 1M0442J05	c 337	9.8	42.6	50	9	AU107432	AU107432 AU107432
c 265	10	43.5	49	12	AZ830102	AZ830102 2M0109B11	c 338	9.8	42.6	50	9	AU108089	AU108089 AU108089
c 266	10	43.5	50	9	AU102361	AU102361 AU102361	339	9.8	42.6	50	10	BI651733	BI651733 603298518
c 267	10	43.5	50	9	AU102877	AU102877 AU102877	c 340	9.8	42.6	50	12	BE882523	BE882523 601507265
c 268	10	43.5	50	9	AU103360	AU103360 AU103360	c 341	9.8	42.6	50	12	AZ665355	AZ665355 1M0546F18
c 269	10	43.5	50	9	AU103481	AU103481 AU103481	c 342	9.8	42.6	50	12	AZ675968	AZ675968 1M0563N12
c 270	10	43.5	50	9	AU104143	AU104143 AU104143	c 343	9.6	41.7	22	9	AA954126	AA954126 qg66a07.s
c 271	10	43.5	50	9	AU104144	AU104144 AU104144	344	9.6	41.7	25	12	AZ511249	AZ511249 1M0356N10
c 272	10	43.5	50	9	AU104466	AU104466 AU104466	345	9.6	41.7	25	12	AZ582580	AZ582580 1M0376N05
c 273	10	43.5	50	9	AU105104	AU105104 AU105104	c 346	9.6	41.7	29	10	BM399121	BM399121 5009-0-53
c 274	10	43.5	50	9	AU105106	AU105106 AU105106	347	9.6	41.7	29	12	AZ508145	AZ508145 1M0350M09
c 275	10	43.5	50	9	AU105108	AU105108 AU105108	348	9.6	41.7	31	12	AZ785133	AZ785133 2M0028J17
c 276	10	43.5	50	9	AU105124	AU105124 AU105124	c 349	9.6	41.7	33	12	BI146188	BI146188 BG02815-5
c 277	10	43.5	50	9	AU105919	AU105919 AU105919	c 350	9.6	41.7	34	9	AA876855	AA876855 nj47D08.s
c 278	10	43.5	50	9	AU107046	AU107046 AU107046	c 351	9.6	41.7	35	12	AZ663930	AZ663930 1M0343N17
c 279	10	43.5	50	9	AU107603	AU107603 AU107603	352	9.6	41.7	35	12	TA386F03Q	TA386F03Q T. brucei
c 280	10	43.5	50	10	BG033307	BG033307 6032298562	353	9.6	41.7	36	10	BI861680	BI861680 603389356
c 281	9.8	42.6	23	12	TA130G06P	TA130G06P 6033030818	c 354	9.6	41.7	37	9	AI683252	AI683252 tx02e12.x
c 282	9.8	42.6	24	12	AZ826609	AZ826609 2M0102P18	c 355	9.6	41.7	37	9	AI721492	AI721492 fc28a01.x
c 283	9.8	42.6	24	12	AZ826609	AZ826609 2M0102P18	c 356	9.6	41.7	37	10	BG976503	BG976503 602846752
c 284	9.8	42.6	25	12	AZ872633	AZ872633 2M0186K01	c 357	9.6	41.7	37	10	BF211603	BF211603 601812103
c 285	9.8	42.6	27	12	AZ422212	AZ422212 1M0200K21	358	9.6	41.7	38	10	BF687876	BF687876 602066947
c 286	9.8	42.6	31	9	AI287914	AI287914 qul3c06.x	c 359	9.6	41.7	40	9	AI118838	AI118838 qd21f12.x
c 287	9.8	42.6	34	9	AI244815	AI244815 q198b02.x	c 360	9.6	41.7	40	9	AI912669	AI912669 we12a07.x
c 288	9.8	42.6	34	9	AI364208	AI364208 qw35h11.x	361	9.6	41.7	40	9	AA238160	AA238160 mx16d10.r
c 289	9.8	42.6	34	9	AI584193	AI584193 fb82a03.x	c 362	9.6	41.7	40	10	BI160469	BI160469 602864532
c 290	9.8	42.6	36	10	BI731533	BI731533 603355235	c 363	9.6	41.7	40	12	AZ998247	AZ998247 2M0485P03
c 291	9.8	42.6	37	9	AI741717	AI741717 wg22b07.x	364	9.6	41.7	41	9	AA665395	AA665395 nu66d05.s
c 292	9.8	42.6	37	12	BI128739	BI128739 G-5n16.f	365	9.6	41.7	41	12	AZ489214	AZ489214 1M0319G22
c 293	9.8	42.6	39	12	AZ774271	AZ774271 2M0003A03	c 366	9.6	41.7	41	12	AZ598587	AZ598587 1M0413A04
c 294	9.8	42.6	39	12	AZ798493	AZ798493 2M0055P15	c 367	9.6	41.7	41	12	AZ832185	AZ832185 2M0112L19
c 295	9.8	42.6	39	12	BI171128	BI171128 SALK_0038	c 368	9.6	41.7	43	9	AA974942	AA974942 on34h12.s
c 296	9.8	42.6	40	9	AI619480	AI619480 ty36g04.x	c 369	9.6	41.7	43	9	AI000393	AI000393 ot06e05.s
c 297	9.8	42.6	40	9	AI628006	AI628006 ty21d06.x	370	9.6	41.7	43	9	AI283782	AI283782 qj75f08.x
c 298	9.8	42.6	40	9	AI720146	AI720146 as78c02.x	371	9.6	41.7	43	9	AI507812	AI507812 sa87e04.y
c 299	9.8	42.6	40	9	AA508464	AA508464 rh66b09.s	c 372	9.6	41.7	43	9	AI663481	AI663481 uk33d07.y
c 300	9.8	42.6	40	12	TA274D05Q	TA274D05Q T. brucei	c 373	9.6	41.7	43	12	AZ465400	AZ465400 1M0275K16
c 301	9.8	42.6	41	12	AZ950920	AZ950920 2M0215L08	374	9.6	41.7	44	9	AV838294	AV838294 AV838294
c 302	9.8	42.6	42	10	BI252223	BI252223 602953127	375	9.6	41.7	44	10	BG035308	BG035308 602324932
c 303	9.8	42.6	42	10	BI252484	BI252484 602952948	c 376	9.6	41.7	44	10	BI918220	BI918220 603183175
c 304	9.8	42.6	42	10	BF206391	BF206391 601869952	c 377	9.6	41.7	44	12	AQ902826	AQ902826 K071087-T
c 305	9.8	42.6	42	12	AZ380365	AZ380365 1M0136F16	c 378	9.6	41.7	44	12	AZ444974	AZ444974 1M0240A01
c 306	9.8	42.6	42	12	AZ785539	AZ785539 2M0029C03	c 379	9.6	41.7	45	10	BJ015280	BJ015280 BJ015280
c 307	9.8	42.6	43	9	AI802246	AI802246 tj36e11.x	c 380	9.6	41.7	45	12	AZ832586	AZ832586 2M0113004
c 308	9.8	42.6	43	12	AZ345882	AZ345882 1M0080016	c 381	9.6	41.7	45	12	TA321E02P	TA321E02P T. brucei
c 309	9.8	42.6	44	10	BM396613	BM396613 5009-0-23	382	9.6	41.7	46	9	AA743588	AA743588 ny29d02.s

383	9.6	41.7	46	10	BI651438	BI651438 603298178	456	9.4	40.9	35	10	BM398446	BM398446 5009-0-45
c 384	9.6	41.7	48	10	W89968	W89968 mf64911.r1	457	9.4	40.9	35	12	AZ616370	AZ616370 IM0446H11
c 385	9.6	41.7	46	10	AL362060	AL362060 AL362060	c 458	9.4	40.9	36	10	BM400508	BM400508 5009-0-74
c 386	9.6	41.7	48	10	R77621	R77621 y176e12.r1	459	9.4	40.9	36	12	AZ487594	AZ487594 IM0317B21
c 387	9.6	41.7	48	12	AZ395292	AZ395292 IM0159C10	460	9.4	40.9	36	12	AZ800990	AZ800990 2M0059H15
c 388	9.6	41.7	49	9	AA724196	AA724196 a109d11.s	461	9.4	40.9	36	12	BH610366	BH610366 SALK_0087
c 389	9.6	41.7	49	9	AA828110	AA828110 OD03C12.S	c 462	9.4	40.9	37	9	AI016514	AI016514 qt30h11.s
c 390	9.6	41.7	49	9	AA990502	AA990502 ua62906.s	463	9.4	40.9	37	9	AI188273	AI188273 qt30h10.x
391	9.6	41.7	49	9	AA995990	AA995990 os13h03.s	c 464	9.4	40.9	37	9	AI619702	AI619702 ty52a05.x
392	9.6	41.7	49	9	AA195871	AA195871 zp98g12.r	c 465	9.4	40.9	37	9	AI634572	AI634572 tz30a01.x
393	9.6	41.7	50	9	AA015340	AA015340 mh13c05.r	c 466	9.4	40.9	37	9	AI796585	AI796585 wh58b02.x
394	9.6	41.7	50	9	AA0102598	AA0102598 AU102598	467	9.4	40.9	37	10	BF130330	BF130330 601818394
395	9.6	41.7	50	9	AU102974	AU102974 AU102974	468	9.4	40.9	38	10	BM399387	BM399387 5009-0-57
396	9.6	41.7	50	9	AU102976	AU102976 AU102976	c 469	9.4	40.9	38	10	BF137365	BF137365 601780736
397	9.6	41.7	50	9	AU102978	AU102978 AU102978	c 470	9.4	40.9	39	10	BE729880	BE729880 601564916
398	9.6	41.7	50	9	AU102979	AU102979 AU102979	471	9.4	40.9	39	12	AZ771052	AZ771052 IM0572P22
399	9.6	41.7	50	9	AU103070	AU103070 AU103070	472	9.4	40.9	40	9	AI123084	AI123084 ok37f03.s
400	9.6	41.7	50	9	AU103432	AU103432 AU103432	c 473	9.4	40.9	40	9	AI800161	AI800161 tr23b08.x
401	9.6	41.7	50	9	AU104418	AU104418 AU104418	474	9.4	40.9	40	10	BG032379	BG032379 602301364
402	9.6	41.7	50	9	AU104428	AU104428 AU104428	475	9.4	40.9	40	10	BM397619	BM397619 5009-0-35
403	9.6	41.7	50	9	AU104681	AU104681 AU104681	c 476	9.4	40.9	40	10	R17398	R17398 yg03d05.r1
404	9.6	41.7	50	9	AU104700	AU104700 AU104700	477	9.4	40.9	40	10	R55306	R55306 y177f05.s1
c 405	9.6	41.7	50	9	AU104732	AU104732 AU104732	c 478	9.4	40.9	40	10	T51935	T51935 yb28c09.s1
c 406	9.6	41.7	50	9	AU104896	AU104896 AU104896	c 479	9.4	40.9	40	12	AZ434256	AZ434256 IM0220L05
c 407	9.6	41.7	50	9	AU104899	AU104899 AU104899	480	9.4	40.9	40	12	BH628364	BH628364 1007079C1
408	9.6	41.7	50	9	AU105190	AU105190 AU105190	481	9.4	40.9	41	10	D74277	D74277 CELK079AXF
409	9.6	41.7	50	9	AU105191	AU105191 AU105191	c 482	9.4	40.9	41	12	AZ848135	AZ848135 2M0149A09
410	9.6	41.7	50	9	AU105192	AU105192 AU105192	483	9.4	40.9	41	12	AZ50920	AZ50920 2M0215L08
411	9.6	41.7	50	9	AU105193	AU105193 AU105193	484	9.4	40.9	42	9	AV838404	AV838404 AV838404
c 412	9.6	41.7	50	9	AU106834	AU106834 AU106834	c 485	9.4	40.9	42	9	AW250581	AW250581 2821639.5
c 413	9.6	41.7	50	9	AU106838	AU106838 AU106838	c 486	9.4	40.9	42	10	BG574349	BG574349 602596276
c 414	9.6	41.7	50	9	AU107016	AU107016 AU107016	c 487	9.4	40.9	42	10	H79257	H79257 yu48b02.s1
c 415	9.6	41.7	50	9	AU107176	AU107176 AU107176	488	9.4	40.9	42	10	T17558	T17558 mps v145.Th
c 416	9.6	41.7	50	9	AU107177	AU107177 AU107177	c 489	9.4	40.9	42	12	AZ628072	AZ628072 IM0480A05
417	9.6	41.7	50	9	AU107613	AU107613 AU107613	c 490	9.4	40.9	43	9	AA910920	AA910920 ok67h09.s
c 418	9.6	41.7	50	10	F37839	F37839 HSPD06947.H	491	9.4	40.9	43	9	AI088505	AI088505 qbl7f07.x
c 419	9.6	41.7	50	12	AF087243	AF087243 AF087243	492	9.4	40.9	43	9	AA134736	AA134736 zm79g03.r
c 420	9.6	41.7	50	12	AZ427184	AZ427184 IM0209D02	c 493	9.4	40.9	43	9	AA134736	AA134736 zm79g03.r
c 421	9.6	41.7	50	12	AZ565607	AZ565607 211PVA09	c 494	9.4	40.9	43	9	AI421857	AI421857 tf55e11.x
c 422	9.6	41.7	50	12	AZ654289	AZ654289 IM0528E22	c 495	9.4	40.9	43	9	AA450033	AA450033 zx35a06.s
c 423	9.6	41.7	50	12	AZ817068	AZ817068 2M0086C07	496	9.4	40.9	43	12	AZ598505	AZ598505 IM0413B21
c 424	9.4	40.9	20	10	BM401265	BM401265 5009-0-85	497	9.4	40.9	44	10	H44436	H44436 y075b02.s1
c 425	9.4	40.9	21	12	AZ410517	AZ410517 IM0183W02	498	9.4	40.9	44	12	BH619955	BH619955 1007063H1
c 426	9.4	40.9	22	10	BM398778	BM398778 5009-0-5-	499	9.4	40.9	45	10	BM395809	BM395809 5009-0-12
c 427	9.4	40.9	23	12	AZ309209	AZ309209 IM0013F14	c 500	9.4	40.9	46	9	AA748313	AA748313 oa54b08.s
c 428	9.4	40.9	23	12	AZ448352	AZ448352 IM0246A06	c 501	9.4	40.9	46	9	AI355632	AI355632 qt76h04.x
c 429	9.4	40.9	24	10	BM400107	BM400107 5009-0-66	502	9.4	40.9	46	9	AI521423	AI521423 th60d09.x
c 430	9.4	40.9	24	12	AZ370614	AZ370614 IM0121010	c 503	9.4	40.9	46	9	AA244435	AA244435 nc07f09.s
c 431	9.4	40.9	24	12	AZ825913	AZ825913 2M0101B22	c 504	9.4	40.9	46	10	R07615	R07615 ye98a03.s1
c 432	9.4	40.9	26	12	AZ377143	AZ377143 IM0131017	c 505	9.4	40.9	46	12	AZ772856	AZ772856 IM0584M01
433	9.4	40.9	26	12	AZ600116	AZ600116 IM0416K16	c 506	9.4	40.9	46	12	BH169798	BH169798 SALK_0019
434	9.4	40.9	27	10	BM397484	BM397484 5009-0-33	c 507	9.4	40.9	46	12	BH624826	BH624826 1007111H0
c 435	9.4	40.9	28	9	AI376644	AI376644 te63b01.x	c 508	9.4	40.9	47	10	BG777442	BG777442 602664745
c 436	9.4	40.9	28	9	AI434082	AI434082 t141h03.x	c 509	9.4	40.9	47	12	TA107C12Q	TA107C12Q T.brucel
c 437	9.4	40.9	28	12	AZ618065	AZ618065 IM0449D11	c 510	9.4	40.9	48	10	BI906001	BI906001 603062308
c 438	9.4	40.9	28	12	AZ817375	AZ817375 2M0086N20	511	9.4	40.9	48	12	AZ796512	AZ796512 2M0052H18
439	9.4	40.9	29	12	TA380E12Q	TA380E12Q T.brucel	512	9.4	40.9	48	12	TA140E08P	TA140E08P T.brucel
c 440	9.4	40.9	29	12	AZ481100	AZ481100 IM0303D07	c 513	9.4	40.9	49	9	AA684136	AA684136 om33h05.s
441	9.4	40.9	30	12	AZ591789	AZ591789 IM0402P06	c 514	9.4	40.9	49	9	AA907765	AA907765 qf86a10.x
442	9.4	40.9	30	12	TA86E11P	TA86E11P T.brucel	515	9.4	40.9	49	9	AI200287	AI200287 qf86a10.x
443	9.4	40.9	31	2	HSM009800	AL044950 Homo sapi	516	9.4	40.9	49	9	AI416542	AI416542 sal0e02.y
444	9.4	40.9	31	9	AI032194	AI032194 OF96D04.s	517	9.4	40.9	49	9	AI758169	AI758169 ty70c07.x
445	9.4	40.9	31	10	N93307	N93307 zb69d02.s1	518	9.4	40.9	49	9	AI766723	AI766723 w103h12.x
446	9.4	40.9	31	12	AZ357525	AZ357525 IM0099B09	c 519	9.4	40.9	49	9	AA478678	AA478678 zw19g04.r
447	9.4	40.9	32	12	AZ601134	AZ601134 IM0419H13	c 520	9.4	40.9	49	10	BF970220	BF970220 602273453
448	9.4	40.9	33	10	BM396982	BM396982 5009-0-27	521	9.4	40.9	49	10	H22280	H22280 y136b03.r1
449	9.4	40.9	33	10	BM401378	BM401378 5009-0-9-	c 522	9.4	40.9	49	12	AQ073133	AQ073133 EP(3)3707
c 450	9.4	40.9	34	9	AI356596	AI356596 qu21e12.x	523	9.4	40.9	50	9	AU102220	AU102220 AU102220
451	9.4	40.9	34	9	AI610129	AI610129 tp13d02.x	c 524	9.4	40.9	50	9	AU102254	AU102254 AU102254
c 452	9.4	40.9	34	12	AZ763845	AZ763845 IM0559C04	525	9.4	40.9	50	9	AU102339	AU102339 AU102339
c 453	9.4	40.9	34	12	AZ800395	AZ800395 2M0058D23	c 526	9.4	40.9	50	9	AU102598	AU102598 AU102598
c 454	9.4	40.9	34	12	TA48H05Q	TA48H05Q T.brucel	c 527	9.4	40.9	50	9	AU102633	AU102633 AU102633
455	9.4	40.9	35	10	BI686449	BI686449 603312821	c 528	9.4	40.9	50	9	AU102635	AU102635 AU102635

c 675	9.2	40.0	46	12	AZ487839	1M0317F14	748	9.2	40.0	50	9	AU105480	AU105480
c 676	9.2	40.0	47	10	B1110720	602895332	749	9.2	40.0	50	9	AU105679	AU105679
c 677	9.2	40.0	47	10	BJ001441	BJ001441	750	9.2	40.0	50	9	AU106620	AU106620
c 678	9.2	40.0	47	10	BE866303	601678950	751	9.2	40.0	50	9	AU106924	AU106924
c 679	9.2	40.0	47	12	BE606685	1M0428A17	c 752	9.2	40.0	50	9	AU107547	AU107547
c 680	9.2	40.0	47	12	TA100F09Q	AL459357 T. brucei	c 753	9.2	40.0	50	9	AU108055	AU108055
c 681	9.2	40.0	47	12	TA330G01P	AL454118 T. brucei	c 754	9.2	40.0	50	9	AV676321	AV676321
c 682	9.2	40.0	47	12	TA324E04Q	AL490992 T. brucei	c 755	9.2	40.0	50	9	AW637027	AW637027
c 683	9.2	40.0	48	9	AA930873	AA930873 vz71e07.s	756	9.2	40.0	50	9	AA554519	AA554519
c 684	9.2	40.0	48	9	AI172854	AI172854 ucl0c07.r	c 757	9.2	40.0	50	10	BG938916	BG938916
c 685	9.2	40.0	48	9	AA386692	AA386692 vb55c05.r	c 758	9.2	40.0	50	10	BI665523	BI665523
c 686	9.2	40.0	48	9	AA484789	AA484789 ng09a11.s	c 759	9.2	40.0	50	10	D21029	D21029
c 687	9.2	40.0	48	10	BI697515	BI697515 603349071	c 760	9.2	40.0	50	10	BE311372	BE311372
c 688	9.2	40.0	48	10	BI829440	BI829440 603080458	c 761	9.2	40.0	50	12	AZ857216	AZ857216
c 689	9.2	40.0	48	12	AZ310125	AZ310125 1M0018M20	762	9.2	40.0	50	12	AZ938271	AZ938271
c 690	9.2	40.0	48	12	BH624836	BH624836 1007089A0	c 763	9.2	40.0	50	12	AZ309156	AZ309156
c 691	9.2	40.0	49	9	AA663894	AA663894 ae74c09.s	c 764	9.2	40.0	50	12	AZ309156	AZ309156
c 692	9.2	40.0	49	9	AA687445	AA687445 ns58g06.s	c 765	9.2	40.0	50	12	BM396464	BM396464
c 693	9.2	40.0	49	9	AA711597	AA711597 v024h02.r	c 766	9.2	40.0	50	12	BM397228	BM397228
c 694	9.2	40.0	49	9	AA902559	AA902559 oJ59b12.s	c 767	9.2	40.0	50	12	BM400927	BM400927
c 695	9.2	40.0	49	9	AI244893	AI244893 qJ98f06.x	768	9.2	40.0	50	12	BM400927	BM400927
c 696	9.2	40.0	49	9	AI308301	AI308301 ts90c10.x	769	9.2	40.0	50	12	BM397858	BM397858
c 697	9.2	40.0	49	9	AA541816	AA541816 n188d08.s	c 770	9.2	40.0	50	12	BM398868	BM398868
c 698	9.2	40.0	49	10	BG519127	BG519127 602578064	c 771	9.2	40.0	50	12	BM399175	BM399175
c 699	9.2	40.0	49	10	U44334	U44334 ENU44334.AS	772	9.2	40.0	50	12	AI565893	AI565893
c 700	9.2	40.0	49	10	BE376178	BE376178 601228534	c 773	9.2	40.0	50	12	AZ307137	AZ307137
c 701	9.2	40.0	49	12	AZ776457	AZ776457 2M0100004	774	9.2	40.0	50	12	AZ361612	AZ361612
c 702	9.2	40.0	49	12	AZ800315	AZ800315 2M0588G16	c 775	9.2	40.0	50	9	AA934268	AA934268
c 703	9.2	40.0	49	12	AZ803036	AZ803036 2M0063M11	c 776	9.2	40.0	50	9	AI560563	AI560563
c 704	9.2	40.0	50	9	AU102219	AU102219	c 777	9.2	40.0	50	9	AZ480819	AZ480819
c 705	9.2	40.0	50	9	AU102279	AU102279	c 778	9.2	40.0	50	9	AZ591905	AZ591905
c 706	9.2	40.0	50	9	AU102280	AU102280	c 779	9.2	40.0	50	9	AZ829200	AZ829200
c 707	9.2	40.0	50	9	AU102532	AU102532	780	9.2	40.0	50	9	AZ843789	AZ843789
c 708	9.2	40.0	50	9	AU102663	AU102663	c 781	9.2	40.0	50	9	AG026067	AG026067
c 709	9.2	40.0	50	9	AU102822	AU102822	c 782	9.2	40.0	50	9	BM398658	BM398658
c 710	9.2	40.0	50	9	AU102827	AU102827	c 783	9.2	40.0	50	9	BM398658	BM398658
c 711	9.2	40.0	50	9	AU102861	AU102861	784	9.2	40.0	50	9	BM398658	BM398658
c 712	9.2	40.0	50	9	AU103032	AU103032	785	9.2	40.0	50	9	BM400355	BM400355
c 713	9.2	40.0	50	9	AU103033	AU103033	c 786	9.2	40.0	50	9	BM400355	BM400355
c 714	9.2	40.0	50	9	AU103037	AU103037	787	9.2	40.0	50	9	AZ394609	AZ394609
c 715	9.2	40.0	50	9	AU103038	AU103038	c 788	9.2	40.0	50	9	AZ783888	AZ783888
c 716	9.2	40.0	50	9	AU103039	AU103039	c 789	9.2	40.0	50	9	AZ792571	AZ792571
c 717	9.2	40.0	50	9	AU103040	AU103040	790	9.2	40.0	50	9	AZ815328	AZ815328
c 718	9.2	40.0	50	9	AU104258	AU104258	791	9.2	40.0	50	9	AI000997	AI000997
c 719	9.2	40.0	50	9	AU104263	AU104263	c 792	9.2	40.0	50	9	AI688077	AI688077
c 720	9.2	40.0	50	9	AU104378	AU104378	c 793	9.2	40.0	50	9	AI767093	AI767093
c 721	9.2	40.0	50	9	AU104390	AU104390	794	9.2	40.0	50	9	AG920609	AG920609
c 722	9.2	40.0	50	9	AU104391	AU104391	c 795	9.2	40.0	50	9	BM400833	BM400833
c 723	9.2	40.0	50	9	AU104394	AU104394	796	9.2	40.0	50	9	BF235989	BF235989
c 724	9.2	40.0	50	9	AU104396	AU104396	c 797	9.2	40.0	50	9	BF532788	BF532788
c 725	9.2	40.0	50	9	AU104397	AU104397	c 798	9.2	40.0	50	9	AZ663905	AZ663905
c 726	9.2	40.0	50	9	AU104398	AU104398	799	9.2	40.0	50	9	AZ809714	AZ809714
c 727	9.2	40.0	50	9	AU104399	AU104399	c 800	9.2	40.0	50	9	AZ818116	AZ818116
c 728	9.2	40.0	50	9	AU104402	AU104402	c 801	9.2	40.0	50	9	BM391939	BM391939
c 729	9.2	40.0	50	9	AU104405	AU104405	802	9.2	40.0	50	9	BI094784	BI094784
c 730	9.2	40.0	50	9	AU104406	AU104406	c 803	9.2	40.0	50	9	BM395935	BM395935
c 731	9.2	40.0	50	9	AU104407	AU104407	c 804	9.2	40.0	50	9	BM396982	BM396982
c 732	9.2	40.0	50	9	AU104409	AU104409	c 805	9.2	40.0	50	9	BM398846	BM398846
c 733	9.2	40.0	50	9	AU104412	AU104412	806	9.2	40.0	50	9	BM398978	BM398978
c 734	9.2	40.0	50	9	AU104413	AU104413	807	9.2	40.0	50	9	AZ311284	AZ311284
c 735	9.2	40.0	50	9	AU104414	AU104414	c 808	9.2	40.0	50	9	AZ324178	AZ324178
c 736	9.2	40.0	50	9	AU104415	AU104415	809	9.2	40.0	50	9	AZ759871	AZ759871
c 737	9.2	40.0	50	9	AU104416	AU104416	c 810	9.2	40.0	50	9	AI241642	AI241642
c 738	9.2	40.0	50	9	AU104417	AU104417	c 811	9.2	40.0	50	9	AI362411	AI362411
c 739	9.2	40.0	50	9	AU104419	AU104419	812	9.2	40.0	50	9	AI368216	AI368216
c 740	9.2	40.0	50	9	AU104422	AU104422	813	9.2	40.0	50	9	AI444187	AI444187
c 741	9.2	40.0	50	9	AU104423	AU104423	814	9.2	40.0	50	9	AI584572	AI584572
c 742	9.2	40.0	50	9	AU104624	AU104624	c 815	9.2	40.0	50	9	AA441877	AA441877
c 743	9.2	40.0	50	9	AU104698	AU104698	816	9.2	40.0	50	9	BI094785	BI094785
c 744	9.2	40.0	50	9	AU104774	AU104774	c 817	9.2	40.0	50	9	BI913027	BI913027
c 745	9.2	40.0	50	9	AU105027	AU105027	818	9.2	40.0	50	9	BJ061523	BJ061523
c 746	9.2	40.0	50	9	AU105296	AU105296	c 819	9.2	40.0	50	9	BE546481	BE546481
c 747	9.2	40.0	50	9	AU105428	AU105428	c 820	9.2	40.0	50	9	BI094785	BI094785

821	9	39.1	34	12	A7389322	A7389322	1M0149G18	C 894	9	39.1	41	12	AZ990351	AZ990351	2M0274101
822	9	39.1	34	12	AZ599278	AZ599278	1M0414G02	C 895	9	39.1	42	10	BM397149	BM397149	5009-0-29
823	9	39.1	34	12	A762551	A762551	1M0557K02	C 896	9	39.1	42	10	BE899162	BE899162	601681959
824	9	39.1	34	12	A763845	A763845	1M0559C04	C 897	9	39.1	42	12	AZ378074	AZ378074	1M0132K12
825	9	39.1	34	12	A2814665	A2814665	2M0082E02	C 898	9	39.1	43	9	AA754675	AA754675	vu20e01.r
826	9	39.1	34	12	A2832199	A2832199	2M0112P22	C 899	9	39.1	43	9	AI222474	AI222474	q921e08.x
827	9	39.1	34	12	A2875088	A2875088	2M0189N23	C 900	9	39.1	43	9	AI569934	AI569934	tf57r08.x
828	9	39.1	34	12	BH000438	BH000438	2M0288N15	C 901	9	39.1	43	9	AI625677	AI625677	ty59b011.x
829	9	39.1	35	10	BF793800	BF793800	602254477	C 902	9	39.1	43	10	BG819177	BG819177	602781306
830	9	39.1	35	10	B1693679	B1693679	603342387	C 903	9	39.1	43	10	BF582059	BF582059	602099239
831	9	39.1	35	10	C01680	C01680	HUMGS000869	C 904	9	39.1	43	12	AZ378285	AZ378285	1M0133B01
832	9	39.1	35	10	H67588	H67588	Yf61403.r1	C 905	9	39.1	43	12	AZ959428	AZ959428	2M0227P05
833	9	39.1	35	10	BF302658	BF302658	602032522	C 906	9	39.1	44	9	AL663346	AL663346	AL663346
834	9	39.1	35	12	A7377416	A7377416	1M0131F13	C 907	9	39.1	44	10	B1518751	B1518751	6030621933
835	9	39.1	35	12	A7276709	A7276709	2M0010N06	C 908	9	39.1	44	12	A2441185	A2441185	1M0232C01
836	9	39.1	35	12	A2807270	A2807270	2M0070D04	C 909	9	39.1	44	12	BH170618	BH170618	SALK_0031
837	9	39.1	35	12	A2834104	A2834104	2M0116G09	C 910	9	39.1	44	12	BH171655	BH171655	SALK_0046
838	9	39.1	35	12	A2984070	A2984070	2M0265K24	C 911	9	39.1	44	12	BH251020	BH251020	SALK_0108
839	9	39.1	35	12	TA181H07Q	TA181H07Q		C 912	9	39.1	44	12	BH251583	BH251583	SALK_0118
840	9	39.1	36	10	BF339163	BF339163	602038468	C 913	9	39.1	44	12	BH254188	BH254188	SALK_0161
841	9	39.1	36	12	A2974570	A2974570	2M0249P08	C 914	9	39.1	44	12	BH612745	BH612745	SALK_0332
842	9	39.1	36	12	A2991248	A2991248	2M0275O16	C 915	9	39.1	44	12	BH613346	BH613346	SALK_0341
843	9	39.1	37	9	AI520830	AI520830	tj08b09.x	C 916	9	39.1	44	12	BH633361	BH633361	SALK_0421
844	9	39.1	37	9	AI374120	AI374120	u168d12.y	C 917	9	39.1	44	12	BH634038	BH634038	SALK_0439
845	9	39.1	37	9	AI641763	AI641763	fc23g04.x	C 918	9	39.1	45	10	BM395809	BM395809	5009-0-12
846	9	39.1	37	9	AI755616	AI755616	EtESTea38	C 919	9	39.1	45	12	AZ331526	AZ331526	1M0038I21
847	9	39.1	37	9	AA458001	AA458001	vf74g10.r	C 920	9	39.1	45	12	AZ331536	AZ331536	1M0059F04
848	9	39.1	37	10	BG166700	BG166700	602339211	C 921	9	39.1	45	12	AZ843434	AZ843434	1M0310D14
849	9	39.1	37	10	B1669786	B1669786	603293364	C 922	9	39.1	45	12	AZ503949	AZ503949	1M0343L24
850	9	39.1	37	10	B7666183	B7666183	603052811	C 923	9	39.1	45	12	AZ777920	AZ777920	2M0012J13
851	9	39.1	37	10	H27436	H27436	Y167907.s1	C 924	9	39.1	45	12	BH212935	BH212935	SALK_0082
852	9	39.1	37	12	AQ025713	AQ025713	1(2)k0260	C 925	9	39.1	45	12	BH633155	BH633155	SALK_0403
853	9	39.1	37	12	AZ802814	AZ802814	2M0061B21	C 926	9	39.1	45	12	BH633466	BH633466	SALK_0426
854	9	39.1	37	12	BH615019	BH615019	BG01854-5	C 927	9	39.1	46	9	AA729084	AA729084	nW03d07.s
855	9	39.1	38	9	AV837949	AV837949	AV837949	C 928	9	39.1	46	9	AA828199	AA828199	oF05c10.s
856	9	39.1	38	10	BG684760	BG684760	602636457	C 929	9	39.1	46	9	AA867748	AA867748	vx16a12.s
857	9	39.1	38	10	B1859456	B1859456	603388196	C 930	9	39.1	46	9	AA883189	AA883189	aml18b12.s
858	9	39.1	38	10	BM397530	BM397530	5009-0-34	C 931	9	39.1	46	9	AA105291	AA105291	mp36g11.r
859	9	39.1	38	10	BE534187	BE534187	601232196	C 932	9	39.1	46	9	AI669413	AI669413	ty32c05.x
860	9	39.1	38	12	BH618869	BH618869	SALK_0399	C 933	9	39.1	46	9	AI702349	AI702349	t266b10.x
861	9	39.1	39	10	BF978061	BF978061	602147965	C 934	9	39.1	46	9	AA151915	AA151915	z0d02c08.s
862	9	39.1	39	10	BG427606	BG427606	602497043	C 935	9	39.1	46	9	AA206549	AA206549	zq57f01.s
863	9	39.1	39	10	BG431624	BG431624	602499216	C 936	9	39.1	46	9	AV833037	AV833037	AV833037
864	9	39.1	39	10	BG434687	BG434687	602506777	C 937	9	39.1	46	10	BG115566	BG115566	602317256
865	9	39.1	39	10	BG538554	BG538554	602567279	C 938	9	39.1	46	10	BM396739	BM396739	5009-0-24
866	9	39.1	39	10	BG542007	BG542007	602572119	C 939	9	39.1	46	10	BF038767	BF038767	601461268
867	9	39.1	39	10	BG546916	BG546916	602573906	C 940	9	39.1	46	12	AQ025695	AQ025695	l(2)k0100
868	9	39.1	39	10	BG547349	BG547349	602574783	C 941	9	39.1	46	12	AZ991930	AZ991930	2M0276F23
869	9	39.1	39	10	BG614605	BG614605	602642087	C 942	9	39.1	47	10	B1916743	B1916743	603178737
870	9	39.1	39	10	BG921277	BG921277	602824119	C 943	9	39.1	47	10	BE312415	BE312415	601150971
871	9	39.1	39	10	B1818665	B1818665	603033263	C 944	9	39.1	47	12	AZ303823	AZ303823	1M0003005
872	9	39.1	39	10	BM395803	BM395803	5009-0-12	C 945	9	39.1	47	12	BH213678	BH213678	SALK_0095
873	9	39.1	39	10	BF209854	BF209854	601873551	C 946	9	39.1	48	10	B1547258	B1547258	603157123
874	9	39.1	39	10	BF213403	BF213403	601845154	C 947	9	39.1	48	10	B1906001	B1906001	603062308
875	9	39.1	39	10	BF245648	BF245648	6018693581	C 948	9	39.1	48	12	AZ781794	AZ781794	2M00231J21
876	9	39.1	39	12	AZ877564	AZ877564	2M0192K05	C 949	9	39.1	48	12	AZ794273	AZ794273	2M0048B01
877	9	39.1	39	12	TA32F04Q	TA32F04Q		C 950	9	39.1	48	12	AZ929474	AZ929474	479.gif26
878	9	39.1	39	12	TA352H03Q	TA352H03Q		C 951	9	39.1	48	12	BH625444	BH625444	1007107D0
879	9	39.1	40	9	AA641270	AA641270	nr78a04.s	C 952	9	39.1	49	9	AA657082	AA657082	VS23C09.r
880	9	39.1	40	9	AA846437	AA846437	al85c09.s	C 953	9	39.1	49	9	AA934271	AA934271	SWOVL3CAN
881	9	39.1	40	9	AA922477	AA922477	om63f09.s	C 954	9	39.1	49	9	AA992903	AA992903	ot92B04.s
882	9	39.1	40	9	AI001093	AI001093	os94c01.s	C 955	9	39.1	49	9	AI142280	AI142280	qr63c10.r
883	9	39.1	40	9	AA160572	AA160572	2q46d11.r	C 956	9	39.1	49	9	AA146415	AA146415	mr66c08.r
884	9	39.1	40	9	AA255159	AA255159	w823c08.r	C 957	9	39.1	49	9	AI424311	AI424311	te90b05.x
885	9	39.1	40	10	BG037009	BG037009	6028287258	C 958	9	39.1	49	9	AI434488	AI434488	t145e03.x
886	9	39.1	40	10	BG912856	BG912856	6028074422	C 959	9	39.1	49	9	AI440059	AI440059	t161f10.x
887	9	39.1	40	10	T90338	Yel16h01.s1		C 960	9	39.1	49	9	AI453675	AI453675	tj28h04.x
888	9	39.1	40	10	BF340179	BF340179	602036555	C 961	9	39.1	49	9	AI652389	AI652389	wb20e07.x
889	9	39.1	40	12	AZ802548	AZ802548	2M0061C05	C 962	9	39.1	49	9	AI760858	AI760858	w109b11.x
890	9	39.1	40	12	BH533074	BH533074	100706080	C 963	9	39.1	49	9	AI800417	AI800417	tj14b07.x
891	9	39.1	41	10	BG251287	BG251287	602366120	C 964	9	39.1	49	9	AI889232	AI889232	wm36b09.x
892	9	39.1	41	10	HI4824	Ym25407.s1		C 965	9	39.1	49	10	BG342381	BG342381	602374108
893	9	39.1	41	12	AZ868291	AZ868291	2M0179Q23	C 966	9	39.1	49	10	B1523939	B1523939	603051683

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c 967 9 39.1 49 10 BJ064738 BJ064738
968 9 39.1 49 10 BM176425 TgESTzyb3
969 9 39.1 49 12 AZ472469 1M0387P09
970 9 39.1 49 12 AZ622361 1M0459B09
c 971 9 39.1 49 12 AZ834261 2M0116G19
972 9 39.1 49 12 BH172699
973 9 39.1 49 12 TA61H08Q
c 974 9 39.1 50 9 AU102278 T. brucei
c 975 9 39.1 50 9 AU102486
c 976 9 39.1 50 9 AU102488 AU102488
c 977 9 39.1 50 9 AU102490 AU102490
c 978 9 39.1 50 9 AU102491 AU102491
c 979 9 39.1 50 9 AU102492 AU102492
c 980 9 39.1 50 9 AU102493 AU102493
c 981 9 39.1 50 9 AU102494 AU102494
c 982 9 39.1 50 9 AU102495 AU102495
c 983 9 39.1 50 9 AU102496 AU102496
c 984 9 39.1 50 9 AU102497 AU102497
c 985 9 39.1 50 9 AU102498 AU102498
c 986 9 39.1 50 9 AU102499 AU102499
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c 990 9 39.1 50 9 AU102503 AU102503
c 991 9 39.1 50 9 AU102508 AU102508
c 992 9 39.1 50 9 AU102509 AU102509
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c 994 9 39.1 50 9 AU102848 AU102848
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c 997 9 39.1 50 9 AU102915 AU102915
c 998 9 39.1 50 9 AU102916 AU102916
c 999 9 39.1 50 9 AU102917 AU102917
1000 9 39.1 50 9 AU102920 AU102920
```

ALIGNMENTS

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RESULT 1
BG545479 32 bp mRNA linear EST 04-APR-2001
LOCUS 602572715F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4701099 5',
DEFINITION mRNA sequence.
ACCESSION BG545479
VERSION BG545479.1 GI:13544144
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-f@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1CM1535 row: m column: 04
High quality sequence stop: 32.
Location/Qualifiers
1. 32
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4701099"
/clone_lib="NIH_MGC_77"
/lab_host="DH10B (T1 phage-resistant)"
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FEATURES

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source
c 967 9 39.1 49 10 BJ064738 BJ064738
968 9 39.1 49 10 BM176425 TgESTzyb3
969 9 39.1 49 12 AZ472469 1M0387P09
970 9 39.1 49 12 AZ622361 1M0459B09
c 971 9 39.1 49 12 AZ834261 2M0116G19
972 9 39.1 49 12 BH172699
973 9 39.1 49 12 TA61H08Q
c 974 9 39.1 50 9 AU102278 T. brucei
c 975 9 39.1 50 9 AU102486
c 976 9 39.1 50 9 AU102488 AU102488
c 977 9 39.1 50 9 AU102490 AU102490
c 978 9 39.1 50 9 AU102491 AU102491
c 979 9 39.1 50 9 AU102492 AU102492
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c 987 9 39.1 50 9 AU102500 AU102500
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c 996 9 39.1 50 9 AU102850 AU102850
c 997 9 39.1 50 9 AU102915 AU102915
c 998 9 39.1 50 9 AU102916 AU102916
c 999 9 39.1 50 9 AU102917 AU102917
1000 9 39.1 50 9 AU102920 AU102920
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```
/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site_1:
SfiI (ggcgctcgcc); Site_2: SfiI (ggcattatggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGCGCATATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCCGCGGCGGCACATG-dT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.9
kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."
```

```
BASE COUNT 5 a 10 c 13 g 4 t
ORIGIN
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Query Match 62.6%; Score 14.4; DB 10; Length 32;
Best Local Similarity 93.8%; Pred. No. 9.3e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Oy 2 ccaggcgctctcggtggg 17
|||||
Db 14 CCAGGCGTCTCGGGG 29
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RESULT 2

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AU106915 50 bp mRNA linear EST 30-AUG-2001
LOCUS AU106915 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION HEP05791, mRNA sequence.
```

```
ACCESSION AU106915
VERSION AU106915.1 GI:13556436
KEYWORDS EST.
```

SOURCE

```
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
```

```
REFERENCE 1 (bases 1 to 50)
AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata
,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki
,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
```

```
EMBO Rep. 2 (5), 388-393 (2001)
21270072
```

JOURNAL

MEDLINE

COMMENT

Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzukl@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
,S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES

source

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1. 50
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="HEP05791"
/clone_lib="Sugano Homo sapiens cDNA library"
BASE COUNT 7 a 12 c 21 g 10 t
ORIGIN
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Query Match 60.9%; Score 14; DB 9; Length 50;
Best Local Similarity 77.3%; Pred. No. 1.6e+04;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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```
Oy 2 ccaggcgctctcggtggccacat 23
|||
Db 14 CCTGGCGTCTGCTGGGGCACCT 35
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RESULT 3

```
AI097023 34 bp mRNA linear EST 20-AUG-1998
LOCUS AI097023
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DEFINITION      oz22e03.x1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone
IMAGE:1676092 3' similar to TR:O15141 O15141 DAXX ;, mRNA sequence.
ACCESSION       AI097023
VERSION         AI097023.1 GI:3446605
KEYWORDS        EST.
SOURCE          human.
ORGANISM        Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE       1 (bases 1 to 34)
AUTHORS         NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE           National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                Tumor Gene Index
JOURNAL         Unpublished (1997)
COMMENT         Contact: Robert Strausberg, Ph.D.
                Email: cgabs-r@mail.nih.gov
                This clone is available royalty-free through LLNL; contact the
                IMAGE Consortium (info@image.llnl.gov) for further information.
                Seq primer: -40ml3 fwd. ET from Amersham
                High quality sequence stop: 1.
FEATURES        1. .34
                Location/Qualifiers
                ..
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
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                /dev_stage="8-9 weeks"
                /lab_host="DH10B"
                /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                was prepared from mRNA obtained from pooled 8-9 week
                (total) fetus material with a Not I - oligo(dT) primer [5',
                TGTTCACCAATCTGAAGTGGGAGCGCGCTTAATTTTCTTTTCTTTT 3'].
                Double-stranded cDNA was ligated to Eco RI adaptors
                (Pharmacia), digested with Not I and cloned into the Not I
                and Eco RI sites of the modified pT73 vector. Library
                went through one round of normalization, and was
                constructed by Bento Soares and M. Fatima Bonaldo. "
BASE COUNT      6 a      8 c      7 g      13 t
ORIGIN          59.1%; Score 13.6; DB 9; Length 34;
                Best Local Similarity 80.0%; Pred. No. 2.1e+04;
                Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      4 aggcgtctcgtggccacat 23
        ||||| || ||||| || ||
Db      2 AGCGTTTCTCTGGGCATAT 21

RESULT      4
AI537615/c  34 bp mRNA linear EST 18-MAR-1999
LOCUS       tp05d08.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2186895 3'
DEFINITION similar to TR:Q26634 Q26634 ALPHA-1 COLLAGEN. ;, mRNA sequence.
ACCESSION   AI537615
VERSION     AI537615.1 GI:4451750
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 34)
AUTHORS     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE       National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
JOURNAL     Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgabs-r@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
            cDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: NCI-CGAP clone distribution information can be
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
FEATURES        1. .34
                Location/Qualifiers
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                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone="IMAGE:2186895"
                /clone_lib="NCI_CGAP_Gas4"
                /tissue_type="poorly differentiated adenocarcinoma with
                signet ring cell features"
                /lab_host="DH10B"
                /note="Organ: stomach; Vector: pCMV-SPORT6; Site_1: SalI;
                Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
                Average insert size 1.69 kb. Life Technologies catalog #:
                11549-011"
BASE COUNT      6 a      16 c      12 g      0 t
ORIGIN          57.4%; Score 13.2; DB 9; Length 34;
                Best Local Similarity 83.3%; Pred. No. 3.2e+04;
                Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

.QY      2 ccaggcgtctcgtggccc 19
        || || ||||| |||||
Db      19 CCCGGGCTCTCGTGGCC 2

RESULT      5
AI102952
LOCUS       AU102952 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION COLFI788, mRNA sequence.
ACCESSION   AU102952
VERSION     AU102952.1 GI:13552473
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 50)
AUTHORS     Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata
            ,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki
            ,Y., Nakamura,Y., Suyama,A. and Sugano,S.
            Diverse transcriptional initiation revealed by fine, large-scale
            mapping of mRNA start sites
            EMBO Rep. 2 (5), 388-393 (2001)
JOURNAL     21270072
MEDLINE
COMMENT     Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
            Email: ysuzuki@ims.u-tokyo.ac.jp
            Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
            ,S. Construction and characterization of a full length-enriched and
            a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES        1. .50
                Location/Qualifiers
                ..
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone="COLFI788"
                /clone_lib="Sugano Homo sapiens cDNA library"
BASE COUNT      17 a      11 c      16 g      6 t
ORIGIN

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Query Match      57.4%; Score 13.2; DB 9; Length 50;
Best Local Similarity 83.3%; Pred. No. 3.6e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 6 gcgtctcgtggccacat 23
||||| ||| ||||| |||||
Db 33 GAGTATCGCGGCCACAT 50

RESULT 6
LOCUS AU106296/c
DEFINITION AU106296 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
KAT06033, mRNA sequence.
ACCESSION AU106296
VERSION AU106296.1 GI:13555817
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 50)
AUTHORS Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata
,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki
,Y., Nakamura,Y., Suyama,A. and Sugano,S.
TITLE Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
JOURNAL EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE 21270072
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yzuku@iims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
,S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES
source
1..50
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="KAT06033"
/clone_lib="Sugano Homo sapiens cDNA library"
BASE COUNT 12 a 11 c 16 g 11 t
ORIGIN

Query Match      57.4%; Score 13.2; DB 9; Length 50;
Best Local Similarity 83.3%; Pred. No. 3.6e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 accaggcgtctcgtggcc 18
||||| ||| ||||| |||||
Db 30 ACAAGGCTCTCTTGGTC 13

RESULT 7
LOCUS T64778/c
DEFINITION T64778 44 bp mRNA linear EST 20-FEB-1995
Yc25h10.r1 Stratagene liver (#937224) Homo sapiens cDNA clone
IMAGE:81763 5', similar to gb:M14058 COMPLEMENT C1R COMPONENT
PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION T64778
VERSION T64778.1 GI:673823
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 44)
AUTHORS Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chitapelli,B.,
Chissee,S., Dietrich,N., Dubuque,T., Favello,A., Gish,W., Hawkins
,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore

B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T.,
Schellenberg,K., Soares,B.B., Tan,F., Thierry-Mieg,J., Trevaskis,E.,
Underwood,K., Wohlmann,P., Waterston,R., Wilson,R. and Marra,M.
Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
97044478
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: estewatson.wustl.edu
Insert Size: 57
High quality sequence starts: 1 High quality sequence stops: 1
Source: IMAGE Consortium, LLNL This clone is available royalty-free
through LLNL ; Contact the IMAGE Consortium (info@image.llnl.gov)
for further information. Trace considered overall poor quality
Insert Length: 57 Std Error: 0.00
Seq primer: M13RP1
High quality sequence stop: 1.
FEATURES
Location/Qualifiers
1..44
/organism="Homo sapiens"
/db_xref="GDB:498820"
/db_xref="taxon:9606"
/clone="IMAGE:81763"
/clone_lib="Stratagene liver (#937224)"
/sex="male"
/dev_stage="49 years old"
/lab_host="SOLR cells (kanamycin resistant)"
/note="Organ: liver; Vector: pBluescript SK; Site_1: EcoRI
; Site_2: XhoI; Cloned unidirectionally. Primer: Oligo
dt. Hepatectomy from normal male caucasian. Average insert
size: 1.1 kb; Uni-ZAP XR Vector: -5' adaptor sequence: 5'
GAATTCGGCAG 3' -3' adaptor sequence: 5'
CTCGAGTTTTTTTTTTTTTTT 3'"
BASE COUNT 5 a 13 c 12 g 11 t 3 others
ORIGIN

Query Match      56.5%; Score 13; DB 10; Length 44;
Best Local Similarity 59.6%; Pred. No. 4.3e+04;
Matches 16; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 accaggcgtctcgtggccacat 23
||||| | | |||||
Db 37 ACCAGGAGNNACAAGGCCACAT 15

RESULT 8
LOCUS BM395935
DEFINITION BM395935 32 bp mRNA linear EST 17-JAN-2002
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION BM395935
VERSION BM395935.1 GI:18195988
KEYWORDS EST.
SOURCE Tetrahymena thermophila.
ORGANISM Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE 1 (bases 1 to 32)
AUTHORS Turkewitz,A.P., Karrer,K.M., Jahn,C., Orlas,E., Kirk,K.E., Frankel
,J. and Klobutcher,L.
EST from Tetrahymena thermophila, strain CU428.1, growing cells
Unpublished (2002)
Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu

```

```
FEATURES
Source
Seq primer: T3.
Location/Qualifiers
1..32
/organism="Tetrahyena thermophila"
/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: Bluescript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."
BASE COUNT      4 a 13 c 11 g 4 t
ORIGIN

Query Match      54.8%; Score 12.6; DB 10; Length 32;
Best Local Similarity 78.9%; Pred. No. 5.8e+04;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 accaggcgtctcgtgggcc 19
||||| ||||| |||||
Db 7 ACCACGCGTGGCGGCC 25

RESULT 9
AI685223
LOCUS      wc70e01.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2323992 3'
DEFINITION similar to SW:GC3_HUMAN P01860 IG GAMMA-3 CHAIN C REGION ;, mRNA
sequence.
ACCESSION  AI685223
VERSION     AI685223.1 GI:4896517
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 43)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Life Technologies catalog #: 11548-013
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Trace considered overall poor quality
Insert Length: 815 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
1..43
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2323992"
/clone_lib="NCI_CGAP_Pan1"
/tissue_type="adenocarcinoma"
/lab_host="DH10B"
/note="Organ: pancreas; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.72 kb. Life Technologies catalog #:
11548-013"
BASE COUNT      11 a 11 c 19 g 2 t
ORIGIN

Query Match      54.8%; Score 12.6; DB 9; Length 43;
Best Local Similarity 78.9%; Pred. No. 6.4e+04;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

FEATURES
source
Seq primer: T3.
Location/Qualifiers
1..32
/organism="Tetrahyena thermophila"
/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: Bluescript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."
BASE COUNT      4 a 13 c 11 g 4 t
ORIGIN

Query Match      54.8%; Score 12.6; DB 9; Length 50;
Best Local Similarity 78.9%; Pred. No. 6.7e+04;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 ggcgctctcgtgggccacat 23
||||| ||||| |||||
Db 13 GGCCTCTCTGTGGGCACCT 31

RESULT 11
AI106917
LOCUS      AU106917 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION HRC07960, mRNA sequence.
ACCESSION  AU106917
VERSION     AU106917.1 GI:13556438
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 50)
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata
,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki
,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@iims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
,S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
Location/Qualifiers
1..50
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CAS07931"
/clone_lib="Sugano Homo sapiens cDNA library"
BASE COUNT      9 a 11 c 22 g 8 t
ORIGIN

Query Match      54.8%; Score 12.6; DB 9; Length 50;
Best Local Similarity 78.9%; Pred. No. 6.7e+04;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 ggcgctctcgtgggccacat 23
||||| ||||| |||||
Db 13 GGCCTCTCTGTGGGCACCT 31

RESULT 11
AI106917
LOCUS      AU106917 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION HRC07960, mRNA sequence.
ACCESSION  AU106917
VERSION     AU106917.1 GI:13556438
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 50)
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata
,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki
,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
Contact: Yutaka Suzuki
```

Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano
S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES

source

1. .50
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="HRC07960"
/clone_lib="Sugano Homo sapiens cDNA library"
8 a 11 c 23 g 8 t

BASE COUNT

ORIGIN

Query Match 54.8%; Score 12.6; DB 9; Length 50;
Best Local Similarity 78.9%; Pred. No. 6.7e+04;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 5 ggcgtctcgtgggcacat 23
||||| ||||| |||||
Db 14 GCGCTCTGCTGGGCACCT 32

RESULT 12
AUI06918
LOCUS
DEFINITION
AUI06918 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
EST.
HUI04186, mRNA sequence.
ACCESSION
AUI06918
VERSION
AUI06918.1 GI:13556439
KEYWORDS
EST.
SOURCE
human.

ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS
Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata
H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki
Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
21270072
COMMENT
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano
S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES

source

1. .50
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="HSI04186"
/clone_lib="Sugano Homo sapiens cDNA library"
7 a 10 c 24 g 9 t

BASE COUNT

ORIGIN

Query Match 54.8%; Score 12.6; DB 9; Length 50;
Best Local Similarity 78.9%; Pred. No. 6.7e+04;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 5 ggcgtctcgtgggcacat 23
||||| ||||| |||||
Db 16 GCGCTCTGCTGGGCACCT 34

RESULT 13

AUI06920

LOCUS

DEFINITION
AUI06920 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone

EST.
HSI05986, mRNA sequence.

ACCESSION
AUI06920

VERSION
AUI06920.1 GI:13556441

KEYWORDS
EST.

SOURCE
human.

ORGANISM
Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1 (bases 1 to 50)

AUTHORS
Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J., Hata
H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki
Y., Nakamura, Y., Suyama, A. and Sugano, S.

TITLE
Diverse transcriptional initiation revealed by fine, large-scale

mapping of mRNA start sites

EMBO Rep. 2 (5), 388-393 (2001)

21270072

COMMENT
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and Sugano
S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES

source

1. .50
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/db_xref="taxon:9606"
/clone="HSI05986"
/clone_lib="Sugano Homo sapiens cDNA library"
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BASE COUNT

ORIGIN

Query Match 54.8%; Score 12.6; DB 9; Length 50;
Best Local Similarity 78.9%; Pred. No. 6.7e+04;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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||||| ||||| |||||
Db 16 GCGCTCTGCTGGGCACCT 34

RESULT 14

AZ789608/c

LOCUS

DEFINITION
AZ789608 Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC2M0037L01 R, DNA sequence.

ACCESSION
AZ789608

VERSION
AZ789608.1 GI:12930609

KEYWORDS
GSS.

SOURCE
house mouse.

ORGANISM
Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
1 (bases 1 to 50)

AUTHORS
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weiss, R.

TITLE
Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

CONTACT: Robert B. Weiss

University of Utah

Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 595 5606

Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0037 row: L column: 01
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 50.
Location/Qualifiers

FEATURES

source

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/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC2M0037L01"
/clone_lib="Mouse 10kb plasmid UUGCLM library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT 13 a 17 c 12 g 8 t
ORIGIN

Query Match 54.8%; Score 12.6; DB 12; Length 50;

Best Local Similarity 78.9%; Pred. No. 6.7e+04; Mismatches 4; Indels 0; Gaps 0;

QY 3 caggcgctctcggtggccac 21

||||| ||||| |||||

Db 27 CTGGCCTGCTGGGCCCC 9

RESULT 15

AZ309417

LOCUS

1M0013G12R Mouse 10kb plasmid UUGCLM library Mus musculus genomic
clone UUGCLM0013G12 R, DNA sequence.

ACCESSION

AZ309417

VERSION

AZ309417.1

KEYWORDS

GSS.

SOURCE

house mouse.

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

1 (bases 1 to 38)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly

M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.

and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0013 row: G column: 12
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 38.
Location/Qualifiers

FEATURES

source

1. .38

/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGCLM0013G12"
/clone_lib="Mouse 10kb plasmid UUGCLM library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gil4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT 8 a 13 c 13 g 4 t
ORIGIN

Query Match 53.9%; Score 12.4; DB 12; Length 38;

Best Local Similarity 72.7%; Pred. No. 7.5e+04;

Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 ccaggcgctctcggtggccacat 23

||||| ||||| |||||

Db 14 CCGGGCCTGACCTGGGGCACAT 35

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Job time: 7012 sec

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